

STN SEARCH HISTORY

FILE 'MEDLINE, BIOSIS, PROMT, SCISEARCH, CAPLUS' ENTERED AT 22:16:05 ON
20 JUL 2006

L1 80110 SEA (HYDROGEN OR H2) (3A) (PRODUC? OR EVOLV? OR GENERAT?)
L2 942 SEA L1 AND (ALGAE OR ALGA OR ALGAL OR CHLAMYDOMONAS OR
REINHARDTII)
L3 24 SEA L2 AND (IRON (A) HYDROGENASE)
L4 14 DUP REM L3 (10 DUPLICATES REMOVED)
L5 5 SEA L4 AND PY<2003
D L5, IBIB ABS, 1-5
L6 39 SEA L2 AND (FE (A) HYDROGENASE)
L7 17 DUP REM L6 (22 DUPLICATES REMOVED)
L8 6 SEA L7 AND PY<2003
L9 4 SEA L8 NOT L5
D L9, IBIB ABS, 1-4

BEST AVAILABLE COPY

STN SEARCH HISTORY

(FILE 'HOME' ENTERED AT 13:21:51 ON 20 JUL 2006)

INDEX 'ADISCTI, ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, ANTE, AQUALINE, AQUASCI, BIOENG, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA, CAPLUS, CEABA-VTB, CIN, CONFSCI, CROPB, CROPU, DDFB, DDFU, DGENE, DISSABS, DRUGB, DRUGMONOG2, DRUGU, EMBAL, EMBASE, ...' ENTERED AT 13:24:27 ON 20 JUL 2006
SEA ((HYDROGEN OR H2) (3A) (PRODUC? OR GENERAT? OR EVOLV?))

39 FILE ADISCTI
10 FILE ADISINSIGHT
12 FILE ADISNEWS
967 FILE AGRICOLA
384 FILE ANABSTR
302 FILE ANTE
544 FILE AQUALINE
509 FILE AQUASCI
1088 FILE BIOENG
9052 FILE BIOSIS
1644 FILE BIOTECHABS
1644 FILE BIOTECHDS
1923 FILE BIOTECHNO
2648 FILE CABA
42097 FILE CAPLUS
3271 FILE CEABA-VTB
1425 FILE CIN
763 FILE CONFSCI
10 FILE CROPB
98 FILE CROPU
60 FILE DDFB
383 FILE DDFU
1207 FILE DGENE
1487 FILE DISSABS
60 FILE DRUGB
634 FILE DRUGU
72 FILE EMBAL
5874 FILE EMBASE
2864 FILE ESBIODBASE
1 FILE FOREGE
463 FILE FROSTI
268 FILE FSTA
25321 FILE GENBANK
116 FILE HEALSAFE
15648 FILE IFIPAT
6 FILE IMSDRUGNEWS
8 FILE IMSRESEARCH
4487 FILE JICST-EPLUS
33 FILE KOSMET
2234 FILE LIFESCI
6006 FILE MEDLINE
4943 FILE NTIS
124 FILE OCEAN
8640 FILE PASCAL
14 FILE PCTGEN
8 FILE PHAR
24 FILE PHARMAML
1 FILE PHIC
60 FILE PHIN
8248 FILE PROMT
10 FILE PROUSDDR
109 FILE RDISCLOSURE
14681 FILE SCISEARCH
10 FILE SYNTHLINE
8353 FILE TOXCENTER
62365 FILE USPATFULL

6028 FILE USPAT2
2 FILE VETB
51 FILE VETU
555 FILE WATER
24599 FILE WPIDS
184 FILE WPIFV
24599 FILE WPINDEX

L1 QUE ((HYDROGEN OR H2) (3A) (PRODUC? OR GENERAT? OR EVOLV?))

FILE 'MEDLINE, BIOSIS, PROMT, SCISEARCH, CAPLUS' ENTERED AT 13:31:07 ON
20 JUL 2006

L2 80084 S (HYDROGEN OR H2) (3A) (PRODUC? OR GENERAT? OR EVOLV?)
L3 1392 S L2 AND (MUTAT? OR MUTEIN OR MUTAG? OR MUTANT)
L4 17 S L3 AND ((IRON OR FE) (A)HYDROGENASE)
L5 13 DUP REM L4 (4 DUPLICATES REMOVED)
L6 4 S L5 AND PY<2003

EAST Search History

| Ref # | Hits | Search Query | DBs | Default Operator | Plurals | Time Stamp |
|-------|-------|---|---|------------------|---------|------------------|
| L1 | 10 | "5871952" | US-PGPUB; USPAT; EPO; JPO; DERWENT | AND | ON | 2006/07/20 21:50 |
| L2 | 2 | "6180406".pn. | US-PGPUB; USPAT; EPO; JPO; DERWENT | AND | ON | 2006/07/20 21:51 |
| L3 | 1113 | light-induced adj promoter | US-PGPUB; USPAT; EPO; JPO; DERWENT | AND | ON | 2006/07/20 21:52 |
| L4 | 1051 | I3 and Chlamydomonas | US-PGPUB; USPAT; EPO; JPO; DERWENT | AND | ON | 2006/07/20 21:52 |
| L5 | 1 | I4 and (hydrogen adj production) | US-PGPUB; USPAT; EPO; JPO; DERWENT | AND | ON | 2006/07/20 22:08 |
| L6 | 71185 | ((hydrogen or H2) adj3 (produc\$4 or generat\$4 or evolv\$4)) | US-PGPUB; USPAT; EPO; JPO; DERWENT | AND | ON | 2006/07/20 22:09 |
| L7 | 955 | L6 and (algae or algal or alga) | US-PGPUB; USPAT; EPO; JPO; DERWENT | AND | ON | 2006/07/20 22:10 |
| L8 | 50 | I7 and (Chlamydomonas or reinhardtii) | US-PGPUB; USPAT; EPO; JPO; DERWENT | AND | ON | 2006/07/20 22:10 |
| L9 | 48 | L8 and (process or method) | US-PGPUB; USPAT; EPO; JPO; DERWENT | AND | ON | 2006/07/20 22:10 |
| L10 | 13 | L9 and ferredoxin | US-PGPUB; USPAT; EPO; JPO; DERWENT | AND | ON | 2006/07/20 22:11 |
| L11 | 22 | L9 and hydrogenase | US-PGPUB; USPAT; EPO; JPO; DERWENT | AND | ON | 2006/07/20 22:11 |

EAST Search History

| | | | | | | |
|-----|------|-------------|---|-----|----|------------------|
| L12 | 11 | l11 not l10 | US-PGPUB; USPAT; EPO; JPO; DERWENT | AND | ON | 2006/07/20 22:11 |
| L13 | 1135 | seibert.in. | US-PGPUB; USPAT; EPO; JPO; DERWENT | AND | ON | 2006/07/20 22:12 |
| L14 | 19 | L13 and l6 | US-PGPUB; USPAT; EPO; JPO; DERWENT | AND | ON | 2006/07/20 22:12 |

EAST Search History

| Ref # | Hits | Search Query | DBs | Default Operator | Plurals | Time Stamp |
|-------|-------|---|---|------------------|---------|------------------|
| L1 | 2 | "4476105".pn. | US-PGPUB; USPAT; EPO; JPO; DERWENT | AND | ON | 2006/07/20 11:31 |
| L2 | 66906 | hydrogen adj3 (produc\$4 or generat\$ or photoproduc\$4 or synthesi\$4) | US-PGPUB; USPAT; EPO; JPO; DERWENT | AND | ON | 2006/07/20 11:33 |
| L3 | 1045 | I2 and (cell adj3 (electroporat\$4 or transform\$4 or transfect\$4 or inject\$4)) | US-PGPUB; USPAT; EPO; JPO; DERWENT | AND | ON | 2006/07/20 11:34 |
| L4 | 779 | I3 and (method SAME (screen\$4 or identif\$4 or select\$4)) | US-PGPUB; USPAT; EPO; JPO; DERWENT | AND | ON | 2006/07/20 11:35 |
| L5 | 840 | I3 and ((method or process) SAME (screen\$4 or identif\$4 or select\$4)) | US-PGPUB; USPAT; EPO; JPO; DERWENT | AND | ON | 2006/07/20 11:36 |
| L6 | 3 | I5 and ((iron or Fe) adj hydrogenase) | US-PGPUB; USPAT; EPO; JPO; DERWENT | AND | ON | 2006/07/20 12:04 |
| L7 | 613 | I5 and oxygen | US-PGPUB; USPAT; EPO; JPO; DERWENT | AND | ON | 2006/07/20 12:04 |
| L8 | 168 | L5 and (algae or alga or algal) | US-PGPUB; USPAT; EPO; JPO; DERWENT | AND | ON | 2006/07/20 12:05 |
| L9 | 18 | L8 and (green adj alg\$4) | US-PGPUB; USPAT; EPO; JPO; DERWENT | AND | ON | 2006/07/20 13:01 |

SCORE Search Results Details for Application 10763712 and Search Result us-10-763-712b-186.rup.

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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: June 29, 2006, 08:19:13 ; Search time 131.333 Seconds
(without alignments)
56.346 Million cell updates/sec

Title: US-10-763-712B-186
Perfect score: 29
Sequence: 1 ADXTIXEE 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries

Database : UniProt_7.2:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|------------|-------|---------------|--------|----|--------------|--------------------|
| 1 | 29 | 100.0 | 219 | 2 | Q66870_9CALI | Q66870 feline cali |
| 2 | 28 | 96.6 | 87 | 2 | Q8P6G5_XANCP | Q8p6g5 xanthomonas |
| 3 | 28 | 96.6 | 191 | 2 | Q445P9_SOLUS | Q445p9 solibacter |
| 4 | 28 | 96.6 | 273 | 2 | Q4KG49_PSEF5 | Q4kg49 pseudomonas |

| | | | | | | |
|----|----|------|------|---|--------------|--------------------|
| 5 | 28 | 96.6 | 319 | 2 | Q5V4C1_HALMA | Q5v4c1 haloarcula |
| 6 | 28 | 96.6 | 414 | 2 | Q93231_CAEEL | Q93231 caenorhabdi |
| 7 | 28 | 96.6 | 516 | 2 | Q564C3_BIFAN | Q564c3 bifidobacte |
| 8 | 28 | 96.6 | 749 | 2 | Q6BZD2_DEBHA | Q6bzd2 debaryomyce |
| 9 | 28 | 96.6 | 817 | 2 | Q6ZPN1_MOUSE | Q6zpn1 mus musculu |
| 10 | 28 | 96.6 | 826 | 2 | Q8IY15_HUMAN | Q8iy15 homo sapien |
| 11 | 28 | 96.6 | 921 | 2 | Q61SM7_CAEER | Q61sm7 caenorhabdi |
| 12 | 28 | 96.6 | 969 | 2 | Q7UM46_RHOBA | Q7um46 rhodopirell |
| 13 | 28 | 96.6 | 1546 | 2 | Q3WJS0_9ACTO | Q3wjs0 frankia sp. |
| 14 | 28 | 96.6 | 1727 | 2 | Q68FD9_MOUSE | Q68fd9 mus musculu |
| 15 | 28 | 96.6 | 1865 | 2 | Q9HCM3_HUMAN | Q9hcm3 homo sapien |
| 16 | 28 | 96.6 | 3463 | 2 | Q7R1E2_GIALA | Q7rle2 giardia lam |
| 17 | 27 | 93.1 | 84 | 2 | Q5RVY2_9HIV1 | Q5rvy2 human immun |
| 18 | 27 | 93.1 | 85 | 2 | Q5RVP5_9HIV1 | Q5rvp5 human immun |
| 19 | 27 | 93.1 | 86 | 2 | Q5RUR7_9HIV1 | Q5rur7 human immun |
| 20 | 27 | 93.1 | 94 | 2 | Q7SJ42_9HIV1 | Q7sj42 human immun |
| 21 | 27 | 93.1 | 94 | 2 | Q7SJ70_9HIV1 | Q7sj70 human immun |
| 22 | 27 | 93.1 | 94 | 2 | Q7SJ73_9HIV1 | Q7sj73 human immun |
| 23 | 27 | 93.1 | 94 | 2 | Q7SJA0_9HIV1 | Q7sja0 human immun |
| 24 | 27 | 93.1 | 94 | 2 | Q7SJB5_9HIV1 | Q7sjb5 human immun |
| 25 | 27 | 93.1 | 94 | 2 | Q7SJG2_9HIV1 | Q7sjg2 human immun |
| 26 | 27 | 93.1 | 96 | 2 | Q6UIH6_9HIV1 | Q6uih6 human immun |
| 27 | 27 | 93.1 | 98 | 2 | Q58RR3_9HIV1 | Q58rr3 human immun |
| 28 | 27 | 93.1 | 98 | 2 | Q5RX46_9HIV1 | Q5rx46 human immun |
| 29 | 27 | 93.1 | 98 | 2 | Q9DPX2_9HIV1 | Q9dpx2 human immun |
| 30 | 27 | 93.1 | 99 | 2 | O09859_9HIV1 | O09859 human immun |
| 31 | 27 | 93.1 | 99 | 2 | O09860_9HIV1 | O09860 human immun |
| 32 | 27 | 93.1 | 99 | 2 | O09861_9HIV1 | O09861 human immun |
| 33 | 27 | 93.1 | 99 | 2 | O09862_9HIV1 | O09862 human immun |
| 34 | 27 | 93.1 | 99 | 2 | O09863_9HIV1 | O09863 human immun |
| 35 | 27 | 93.1 | 99 | 2 | O09865_9HIV1 | O09865 human immun |
| 36 | 27 | 93.1 | 99 | 2 | O09867_9HIV1 | O09867 human immun |
| 37 | 27 | 93.1 | 99 | 2 | O09868_9HIV1 | O09868 human immun |
| 38 | 27 | 93.1 | 99 | 2 | O09869_9HIV1 | O09869 human immun |
| 39 | 27 | 93.1 | 99 | 2 | O09871_9HIV1 | O09871 human immun |
| 40 | 27 | 93.1 | 99 | 2 | O09950_9HIV1 | O09950 human immun |
| 41 | 27 | 93.1 | 99 | 2 | O09951_9HIV1 | O09951 human immun |
| 42 | 27 | 93.1 | 99 | 2 | O09952_9HIV1 | O09952 human immun |
| 43 | 27 | 93.1 | 99 | 2 | O09953_9HIV1 | O09953 human immun |
| 44 | 27 | 93.1 | 99 | 2 | O09954_9HIV1 | O09954 human immun |
| 45 | 27 | 93.1 | 99 | 2 | O09955_9HIV1 | O09955 human immun |
| 46 | 27 | 93.1 | 99 | 2 | O09956_9HIV1 | O09956 human immun |
| 47 | 27 | 93.1 | 99 | 2 | O10196_9HIV1 | O10196 human immun |
| 48 | 27 | 93.1 | 99 | 2 | O10201_9HIV1 | O10201 human immun |
| 49 | 27 | 93.1 | 99 | 2 | O10215_9HIV1 | O10215 human immun |
| 50 | 27 | 93.1 | 99 | 2 | O38681_9HIV1 | O38681 human immun |
| 51 | 27 | 93.1 | 99 | 2 | O38686_9HIV1 | O38686 human immun |
| 52 | 27 | 93.1 | 99 | 2 | Q58RN9_9HIV1 | Q58rn9 human immun |
| 53 | 27 | 93.1 | 99 | 2 | Q58RS6_9HIV1 | Q58rs6 human immun |
| 54 | 27 | 93.1 | 99 | 2 | Q58RS8_9HIV1 | Q58rs8 human immun |
| 55 | 27 | 93.1 | 99 | 2 | Q5RT92_9HIV1 | Q5rt92 human immun |
| 56 | 27 | 93.1 | 99 | 2 | Q5RTF3_9HIV1 | Q5rtf3 human immun |
| 57 | 27 | 93.1 | 99 | 2 | Q5RTF9_9HIV1 | Q5rtf9 human immun |
| 58 | 27 | 93.1 | 99 | 2 | Q5RTG5_9HIV1 | Q5rtg5 human immun |
| 59 | 27 | 93.1 | 99 | 2 | Q5RTH8_9HIV1 | Q5rth8 human immun |
| 60 | 27 | 93.1 | 99 | 2 | Q5RTS8_9HIV1 | Q5rts8 human immun |
| 61 | 27 | 93.1 | 99 | 2 | Q5RUB4_9HIV1 | Q5rub4 human immun |
| 62 | 27 | 93.1 | 99 | 2 | Q5RUB5_9HIV1 | Q5rub5 human immun |
| 63 | 27 | 93.1 | 99 | 2 | Q5RUC6_9HIV1 | Q5ruc6 human immun |
| 64 | 27 | 93.1 | 99 | 2 | Q5RUY4_9HIV1 | Q5rui4 human immun |
| 65 | 27 | 93.1 | 99 | 2 | Q5RUY5_9HIV1 | Q5rui5 human immun |

| | | | | | | | | |
|-----|----|------|----|---|--------------|--------|-------|-------|
| 66 | 27 | 93.1 | 99 | 2 | Q5RVM1_9HIV1 | Q5rvm1 | human | immun |
| 67 | 27 | 93.1 | 99 | 2 | Q5RVP4_9HIV1 | Q5rvp4 | human | immun |
| 68 | 27 | 93.1 | 99 | 2 | Q5RVP6_9HIV1 | Q5rvp6 | human | immun |
| 69 | 27 | 93.1 | 99 | 2 | Q5RW30_9HIV1 | Q5rw30 | human | immun |
| 70 | 27 | 93.1 | 99 | 2 | Q5RW31_9HIV1 | Q5rw31 | human | immun |
| 71 | 27 | 93.1 | 99 | 2 | Q5RW32_9HIV1 | Q5rw32 | human | immun |
| 72 | 27 | 93.1 | 99 | 2 | Q5RW91_9HIV1 | Q5rw91 | human | immun |
| 73 | 27 | 93.1 | 99 | 2 | Q5RW92_9HIV1 | Q5rw92 | human | immun |
| 74 | 27 | 93.1 | 99 | 2 | Q5RWA2_9HIV1 | Q5rwa2 | human | immun |
| 75 | 27 | 93.1 | 99 | 2 | Q5RWA5_9HIV1 | Q5rwa5 | human | immun |
| 76 | 27 | 93.1 | 99 | 2 | Q5RWP2_9HIV1 | Q5rwp2 | human | immun |
| 77 | 27 | 93.1 | 99 | 2 | Q5RWS6_9HIV1 | Q5rws6 | human | immun |
| 78 | 27 | 93.1 | 99 | 2 | Q5RX44_9HIV1 | Q5rx44 | human | immun |
| 79 | 27 | 93.1 | 99 | 2 | Q5RX45_9HIV1 | Q5rx45 | human | immun |
| 80 | 27 | 93.1 | 99 | 2 | Q5RX59_9HIV1 | Q5rx59 | human | immun |
| 81 | 27 | 93.1 | 99 | 2 | Q5RX60_9HIV1 | Q5rx60 | human | immun |
| 82 | 27 | 93.1 | 99 | 2 | Q5RX91_9HIV1 | Q5rx91 | human | immun |
| 83 | 27 | 93.1 | 99 | 2 | Q5RXR9_9HIV1 | Q5rxr9 | human | immun |
| 84 | 27 | 93.1 | 99 | 2 | Q5RYB1_9HIV1 | Q5ryb1 | human | immun |
| 85 | 27 | 93.1 | 99 | 2 | Q5RYC4_9HIV1 | Q5ryc4 | human | immun |
| 86 | 27 | 93.1 | 99 | 2 | Q5RYF1_9HIV1 | Q5ryf1 | human | immun |
| 87 | 27 | 93.1 | 99 | 2 | Q5RYF2_9HIV1 | Q5ryf2 | human | immun |
| 88 | 27 | 93.1 | 99 | 2 | Q5RYF3_9HIV1 | Q5ryf3 | human | immun |
| 89 | 27 | 93.1 | 99 | 2 | Q6Q042_9HIV1 | Q6q042 | human | immun |
| 90 | 27 | 93.1 | 99 | 2 | Q6REF0_9HIV1 | Q6ref0 | human | immun |
| 91 | 27 | 93.1 | 99 | 2 | Q6SMF9_9HIV1 | Q6smf9 | human | immun |
| 92 | 27 | 93.1 | 99 | 2 | Q6UIH5_9HIV1 | Q6uih5 | human | immun |
| 93 | 27 | 93.1 | 99 | 2 | Q6UIH7_9HIV1 | Q6uih7 | human | immun |
| 94 | 27 | 93.1 | 99 | 2 | Q7SPI1_9HIV1 | Q7spi1 | human | immun |
| 95 | 27 | 93.1 | 99 | 2 | Q7SQC0_9HIV1 | Q7sqc0 | human | immun |
| 96 | 27 | 93.1 | 99 | 2 | Q7SQC3_9HIV1 | Q7sqc3 | human | immun |
| 97 | 27 | 93.1 | 99 | 2 | Q7ZCK3_9HIV1 | Q7zck3 | human | immun |
| 98 | 27 | 93.1 | 99 | 2 | Q7ZCK4_9HIV1 | Q7zck4 | human | immun |
| 99 | 27 | 93.1 | 99 | 2 | Q7ZCK5_9HIV1 | Q7zck5 | human | immun |
| 100 | 27 | 93.1 | 99 | 2 | Q7ZCK6_9HIV1 | Q7zck6 | human | immun |
| 101 | 27 | 93.1 | 99 | 2 | Q7ZCK7_9HIV1 | Q7zck7 | human | immun |
| 102 | 27 | 93.1 | 99 | 2 | Q7ZCK8_9HIV1 | Q7zck8 | human | immun |
| 103 | 27 | 93.1 | 99 | 2 | Q7ZCK9_9HIV1 | Q7zck9 | human | immun |
| 104 | 27 | 93.1 | 99 | 2 | Q7ZCL0_9HIV1 | Q7zcl0 | human | immun |
| 105 | 27 | 93.1 | 99 | 2 | Q7ZCL2_9HIV1 | Q7zcl2 | human | immun |
| 106 | 27 | 93.1 | 99 | 2 | Q7ZPC8_9HIV1 | Q7zpc8 | human | immun |
| 107 | 27 | 93.1 | 99 | 2 | Q8ANE7_9HIV1 | Q8ane7 | human | immun |
| 108 | 27 | 93.1 | 99 | 2 | Q8ANG8_9HIV1 | Q8ang8 | human | immun |
| 109 | 27 | 93.1 | 99 | 2 | Q8ANI7_9HIV1 | Q8ani7 | human | immun |
| 110 | 27 | 93.1 | 99 | 2 | Q8ANJ2_9HIV1 | Q8anj2 | human | immun |
| 111 | 27 | 93.1 | 99 | 2 | Q8ANJ8_9HIV1 | Q8anj8 | human | immun |
| 112 | 27 | 93.1 | 99 | 2 | Q8ANK2_9HIV1 | Q8ank2 | human | immun |
| 113 | 27 | 93.1 | 99 | 2 | Q8ANK4_9HIV1 | Q8ank4 | human | immun |
| 114 | 27 | 93.1 | 99 | 2 | Q8ANN9_9HIV1 | Q8ann9 | human | immun |
| 115 | 27 | 93.1 | 99 | 2 | Q8ANP9_9HIV1 | Q8anp9 | human | immun |
| 116 | 27 | 93.1 | 99 | 2 | Q8ANT3_9HIV1 | Q8ant3 | human | immun |
| 117 | 27 | 93.1 | 99 | 2 | Q8ANZ2_9HIV1 | Q8anz2 | human | immun |
| 118 | 27 | 93.1 | 99 | 2 | Q8UNX0_9HIV1 | Q8unx0 | human | immun |
| 119 | 27 | 93.1 | 99 | 2 | Q99D67_9HIV1 | Q99d67 | human | immun |
| 120 | 27 | 93.1 | 99 | 2 | Q99EZ3_9HIV1 | Q99ez3 | human | immun |
| 121 | 27 | 93.1 | 99 | 2 | Q9E105_9HIV1 | Q9e105 | human | immun |
| 122 | 27 | 93.1 | 99 | 2 | Q9E112_9HIV1 | Q9e112 | human | immun |
| 123 | 27 | 93.1 | 99 | 2 | Q9E113_9HIV1 | Q9e113 | human | immun |
| 124 | 27 | 93.1 | 99 | 2 | Q9E3P2_9HIV1 | Q9e3p2 | human | immun |
| 125 | 27 | 93.1 | 99 | 2 | Q9ILQ2_9HIV1 | Q9ilq2 | human | immun |
| 126 | 27 | 93.1 | 99 | 2 | Q9ILU4_9HIV1 | Q9ilu4 | human | immun |

| | | | | | | |
|-----|----|------|-----|---|--------------|--------------------|
| 127 | 27 | 93.1 | 99 | 2 | Q9J017_9HIV1 | Q9j017 human immun |
| 128 | 27 | 93.1 | 99 | 2 | Q9J018_9HIV1 | Q9j018 human immun |
| 129 | 27 | 93.1 | 99 | 2 | Q9JAN4_9HIV1 | Q9jan4 human immun |
| 130 | 27 | 93.1 | 99 | 2 | Q9JAN5_9HIV1 | Q9jan5 human immun |
| 131 | 27 | 93.1 | 99 | 2 | Q9JAN6_9HIV1 | Q9jan6 human immun |
| 132 | 27 | 93.1 | 99 | 2 | Q9JAN7_9HIV1 | Q9jan7 human immun |
| 133 | 27 | 93.1 | 99 | 2 | Q9JAN8_9HIV1 | Q9jan8 human immun |
| 134 | 27 | 93.1 | 99 | 2 | Q9JAN9_9HIV1 | Q9jan9 human immun |
| 135 | 27 | 93.1 | 99 | 2 | Q9JAP0_9HIV1 | Q9jap0 human immun |
| 136 | 27 | 93.1 | 99 | 2 | Q9JAP1_9HIV1 | Q9jap1 human immun |
| 137 | 27 | 93.1 | 99 | 2 | Q9JAP2_9HIV1 | Q9jap2 human immun |
| 138 | 27 | 93.1 | 99 | 2 | Q9JAP4_9HIV1 | Q9jap4 human immun |
| 139 | 27 | 93.1 | 99 | 2 | Q9JAP5_9HIV1 | Q9jap5 human immun |
| 140 | 27 | 93.1 | 100 | 2 | Q58RS1_9HIV1 | Q58rs1 human immun |
| 141 | 27 | 93.1 | 100 | 2 | Q5MHI0_9HIV1 | Q5mhi0 human immun |
| 142 | 27 | 93.1 | 100 | 2 | Q6QJW4_9HIV1 | Q6qjw4 human immun |
| 143 | 27 | 93.1 | 106 | 2 | Q8Q3D8_9HIV1 | Q8q3d8 human immun |
| 144 | 27 | 93.1 | 118 | 2 | Q70VT4_9HIV1 | Q70vt4 human immun |
| 145 | 27 | 93.1 | 143 | 2 | Q3MGN0_ANAVT | Q3mgn0 anabaena va |
| 146 | 27 | 93.1 | 144 | 2 | Q8YUC8_ANASP | Q8yuc8 anabaena sp |
| 147 | 27 | 93.1 | 156 | 2 | Q5Y8C9_9CLOT | Q5y8c9 clostridium |
| 148 | 27 | 93.1 | 156 | 2 | Q68YU5_9CLOT | Q68yu5 uncultured |
| 149 | 27 | 93.1 | 156 | 2 | Q68YV3_9CLOT | Q68yv3 uncultured |
| 150 | 27 | 93.1 | 156 | 2 | Q68YV4_9CLOT | Q68yv4 uncultured |

ALIGNMENTS

RESULT 1

Q66870_9CALI

ID Q66870_9CALI PRELIMINARY; PRT; 219 AA.

AC Q66870;

DT 01-NOV-1996, integrated into UniProtKB/TrEMBL.

DT 01-NOV-1996, sequence version 1.

DT 07-FEB-2006, entry version 19.

DE Capsid protein (Fragment).

OS Feline calicivirus.

OC Viruses; ssRNA positive-strand viruses, no DNA stage; Caliciviridae;

OC Vesivirus.

OX NCBI_TaxID=11978;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=FS;

RX MEDLINE=95028111; PubMed=7941699; DOI=10.1016/0168-1702(94)90016-7;

RA Seal B.S.;

RT "Analysis of capsid protein gene variation among divergent isolates of feline calicivirus.";

RL Virus Res. 33:39-53(1994).

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CC

DR EMBL; U06650; AAA67210.1; -; Genomic_RNA.

DR InterPro; IPR004005; Calici_coat.

DR Pfam; PF00915; Calici_coat; 1.

FT NON_TER 1 1

FT NON_TER 219 219

SQ SEQUENCE 219 AA; 23926 MW; E403FECF5C022469 CRC64;

Query Match 100.0%; Score 29; DB 2; Length 219;

[Score Home Page](#) [Retrieve Application List](#) [SCORE System Overview](#) [SCORE FAQ](#) [Comments / Suggest](#)

This page gives you Search Results detail for the Application 10763712 and Search Result us-10-763712
[start](#)

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: June 29, 2006, 08:24:08 ; Search time 15.6667 Seconds
(without alignments)
49.132 Million cell updates/sec

Title: US-10-763-712B-186
Perfect score: 29
Sequence: 1 ADXTIXEE 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries

Database : PIR_80:*
1: pirl:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|------------|-------|------------------|--------|----|--------|--------------------|
| 1 | 28 | 96.6 | 386 | 2 | T19354 | hypothetical prote |
| 2 | 27 | 93.1 | 144 | 2 | AI2108 | hypothetical prote |
| 3 | 27 | 93.1 | 290 | 2 | H96982 | L-serine dehydrata |
| 4 | 27 | 93.1 | 382 | 2 | JC2571 | cellulase (EC 3.2. |
| 5 | 27 | 93.1 | 574 | 1 | HQCL1P | hydrogenase (EC 1. |
| 6 | 27 | 93.1 | 582 | 2 | D96903 | hydrogene dehydrog |
| 7 | 27 | 93.1 | 582 | 2 | JC6002 | hydrogenase (EC 1. |
| 8 | 27 | 93.1 | 585 | 2 | D57150 | hydrogenase (EC 1. |

| | | | | | | |
|----|----|------|------|---|---------|----------------------|
| 9 | 27 | 93.1 | 608 | 2 | C72405 | hydrogenase (EC 1. |
| 10 | 27 | 93.1 | 1206 | 2 | T18557 | probable hydrogenase |
| 11 | 27 | 93.1 | 4096 | 2 | A57099 | DNA-activated prot |
| 12 | 26 | 89.7 | 99 | 2 | S63716 | HIV-1 retropepsin |
| 13 | 26 | 89.7 | 100 | 2 | S63708 | HIV-1 retropepsin |
| 14 | 26 | 89.7 | 106 | 2 | S63756 | HIV-1 retropepsin |
| 15 | 26 | 89.7 | 113 | 4 | S34484 | retropepsin (EC 3. |
| 16 | 26 | 89.7 | 115 | 2 | S63741 | HIV-1 retropepsin |
| 17 | 26 | 89.7 | 122 | 2 | S63749 | HIV-1 retropepsin |
| 18 | 26 | 89.7 | 123 | 2 | S63744 | HIV-1 retropepsin |
| 19 | 26 | 89.7 | 126 | 2 | S63738 | HIV-1 retropepsin |
| 20 | 26 | 89.7 | 129 | 2 | S63740 | HIV-1 retropepsin |
| 21 | 26 | 89.7 | 129 | 2 | S63739 | HIV-1 retropepsin |
| 22 | 26 | 89.7 | 130 | 2 | S63754 | HIV-1 retropepsin |
| 23 | 26 | 89.7 | 131 | 2 | A59365 | ribosomal protein |
| 24 | 26 | 89.7 | 132 | 2 | S63733 | HIV-1 retropepsin |
| 25 | 26 | 89.7 | 133 | 2 | S63736 | HIV-1 retropepsin |
| 26 | 26 | 89.7 | 143 | 2 | S63735 | HIV-1 retropepsin |
| 27 | 26 | 89.7 | 145 | 2 | S63745 | HIV-1 retropepsin |
| 28 | 26 | 89.7 | 149 | 2 | S63734 | HIV-1 retropepsin |
| 29 | 26 | 89.7 | 154 | 2 | S63751 | HIV-1 retropepsin |
| 30 | 26 | 89.7 | 160 | 2 | S63753 | HIV-1 retropepsin |
| 31 | 26 | 89.7 | 166 | 2 | S63752 | HIV-1 retropepsin |
| 32 | 26 | 89.7 | 176 | 2 | S63747 | HIV-1 retropepsin |
| 33 | 26 | 89.7 | 294 | 2 | S66041 | conserved hypothet |
| 34 | 26 | 89.7 | 297 | 2 | D83825 | hypothetical prote |
| 35 | 26 | 89.7 | 298 | 2 | F83652 | superoxide-inducib |
| 36 | 26 | 89.7 | 332 | 2 | T42370 | probable glucan 1, |
| 37 | 26 | 89.7 | 403 | 2 | H90487 | alpha-fucosidase C |
| 38 | 26 | 89.7 | 407 | 2 | T39282 | probable exo-beta- |
| 39 | 26 | 89.7 | 421 | 1 | HQDVFL | cytochrome-c3 hydr |
| 40 | 26 | 89.7 | 421 | 1 | HQDVLV | cytochrome-c3 hydr |
| 41 | 26 | 89.7 | 463 | 2 | JC2307 | ribulose-bisphosph |
| 42 | 26 | 89.7 | 786 | 2 | H69980 | single-strand DNA- |
| 43 | 26 | 89.7 | 1002 | 1 | GNLJND | HIV-1 retropepsin |
| 44 | 26 | 89.7 | 1002 | 2 | S54378 | pol polyprotein - |
| 45 | 26 | 89.7 | 1003 | 1 | GNVWLTV | HIV-1 retropepsin |
| 46 | 26 | 89.7 | 1003 | 1 | B44001 | HIV-1 retropepsin |
| 47 | 26 | 89.7 | 1003 | 1 | GNVWA2 | HIV-1 retropepsin |
| 48 | 26 | 89.7 | 1012 | 1 | GNVWVL | HIV-1 retropepsin |
| 49 | 26 | 89.7 | 1015 | 1 | GNVWH3 | HIV-1 retropepsin |
| 50 | 26 | 89.7 | 1112 | 2 | T02848 | hsp70-related prot |
| 51 | 26 | 89.7 | 1876 | 2 | E97944 | zinc metalloprotei |
| 52 | 25 | 86.2 | 447 | 2 | T40423 | hypothetical prote |
| 53 | 25 | 86.2 | 581 | 2 | F97184 | DNA modification m |
| 54 | 25 | 86.2 | 668 | 2 | JQ2356 | capsid protein - f |
| 55 | 25 | 86.2 | 716 | 1 | C60008 | RNA-directed RNA p |
| 56 | 25 | 86.2 | 716 | 1 | C60011 | RNA-directed RNA p |
| 57 | 25 | 86.2 | 716 | 1 | P2IV34 | RNA-directed RNA p |
| 58 | 25 | 86.2 | 716 | 1 | P2IV61 | RNA-directed RNA p |
| 59 | 25 | 86.2 | 716 | 1 | P2IVWS | RNA-directed RNA p |
| 60 | 25 | 86.2 | 716 | 1 | P2IV68 | RNA-directed RNA p |
| 61 | 25 | 86.2 | 716 | 2 | S07418 | RNA-directed RNA p |
| 62 | 25 | 86.2 | 1397 | 2 | T51292 | Dna2p - fission ye |
| 63 | 25 | 86.2 | 1398 | 2 | T39568 | hypothetical helic |
| 64 | 24 | 82.8 | 89 | 2 | G70722 | hypothetical prote |
| 65 | 24 | 82.8 | 161 | 1 | HMECA1 | hemagglutinin AFA- |
| 66 | 24 | 82.8 | 204 | 2 | G83911 | hypothetical prote |
| 67 | 24 | 82.8 | 232 | 2 | C95196 | conserved hypothet |
| 68 | 24 | 82.8 | 232 | 2 | H98062 | N-acetylmannosamin |
| 69 | 24 | 82.8 | 232 | 2 | C98021 | N-acetylmannosamin |

| | | | | | | |
|-----|----|------|------|---|--------|--------------------|
| 70 | 24 | 82.8 | 244 | 2 | D86849 | glutamate ABC tran |
| 71 | 24 | 82.8 | 245 | 2 | F64465 | hypothetical prote |
| 72 | 24 | 82.8 | 261 | 2 | T25206 | hypothetical prote |
| 73 | 24 | 82.8 | 262 | 2 | T05287 | ribosomal protein |
| 74 | 24 | 82.8 | 272 | 2 | T01148 | probable acetone-c |
| 75 | 24 | 82.8 | 274 | 2 | AB2325 | hypothetical prote |
| 76 | 24 | 82.8 | 290 | 2 | T47991 | hypothetical prote |
| 77 | 24 | 82.8 | 313 | 2 | E95113 | proteinase maturat |
| 78 | 24 | 82.8 | 313 | 2 | D97982 | proteinase maturat |
| 79 | 24 | 82.8 | 324 | 2 | T34148 | hypothetical prote |
| 80 | 24 | 82.8 | 342 | 2 | C91176 | probable heme/hemo |
| 81 | 24 | 82.8 | 342 | 2 | D86022 | probable heme/hemo |
| 82 | 24 | 82.8 | 400 | 2 | T15459 | hypothetical prote |
| 83 | 24 | 82.8 | 428 | 2 | H86890 | hypothetical prote |
| 84 | 24 | 82.8 | 442 | 1 | UBUTB | tubulin beta chain |
| 85 | 24 | 82.8 | 477 | 2 | A28534 | fatty-acyl-CoA red |
| 86 | 24 | 82.8 | 506 | 2 | F70617 | probable aldehyde |
| 87 | 24 | 82.8 | 526 | 2 | S34945 | nitrogenase (EC 1. |
| 88 | 24 | 82.8 | 569 | 2 | H87926 | protein C17D12.7 [|
| 89 | 24 | 82.8 | 607 | 2 | F71094 | probable aldehyde |
| 90 | 24 | 82.8 | 653 | 2 | D87602 | sensory box histid |
| 91 | 24 | 82.8 | 655 | 2 | A54408 | mannosyl-oligosacc |
| 92 | 24 | 82.8 | 681 | 2 | G90075 | triacylglycerol li |
| 93 | 24 | 82.8 | 682 | 2 | S68970 | triacylglycerol li |
| 94 | 24 | 82.8 | 718 | 2 | A82352 | iron(III) compound |
| 95 | 24 | 82.8 | 732 | 2 | T43619 | secreted protein k |
| 96 | 24 | 82.8 | 732 | 2 | S30060 | protein kinase ypk |
| 97 | 24 | 82.8 | 775 | 2 | T40647 | ubiquitin carboxyl |
| 98 | 24 | 82.8 | 870 | 2 | B40121 | GTPase-activating |
| 99 | 24 | 82.8 | 935 | 2 | T51930 | kinesin [imported] |
| 100 | 24 | 82.8 | 942 | 2 | JC7316 | testicular zinc fi |
| 101 | 24 | 82.8 | 1038 | 2 | JT0663 | ras GTPase-activat |
| 102 | 24 | 82.8 | 1044 | 2 | S01966 | GTPase-activating |
| 103 | 24 | 82.8 | 1047 | 2 | A40121 | GTPase-activating |
| 104 | 24 | 82.8 | 1171 | 2 | A37829 | parasporal crystal |
| 105 | 24 | 82.8 | 1171 | 2 | I40572 | parasporal crystal |
| 106 | 24 | 82.8 | 1224 | 2 | T14007 | microtubule-associ |
| 107 | 24 | 82.8 | 1242 | 2 | S51246 | probable DNA repai |
| 108 | 24 | 82.8 | 1371 | 2 | D82606 | DNA primase XF2061 |
| 109 | 24 | 82.8 | 1374 | 2 | T16129 | hypothetical prote |
| 110 | 24 | 82.8 | 1499 | 2 | AC2555 | hypothetical prote |
| 111 | 24 | 82.8 | 1522 | 2 | T39371 | transcription regu |
| 112 | 24 | 82.8 | 1634 | 2 | T26517 | hypothetical prote |
| 113 | 24 | 82.8 | 1701 | 2 | A26868 | major merozoite su |
| 114 | 24 | 82.8 | 1701 | 2 | A54498 | major merozoite su |
| 115 | 24 | 82.8 | 2238 | 1 | RRVUBY | genome polyprotein |
| 116 | 24 | 82.8 | 2338 | 2 | I73957 | kinase-related pro |
| 117 | 23 | 79.3 | 70 | 2 | A59230 | androgen-binding p |
| 118 | 23 | 79.3 | 70 | 2 | B59230 | androgen-binding p |
| 119 | 23 | 79.3 | 72 | 2 | A46958 | androgen-binding p |
| 120 | 23 | 79.3 | 90 | 2 | H83931 | hypothetical prote |
| 121 | 23 | 79.3 | 102 | 2 | AE1099 | B. subtilis SpoVG |
| 122 | 23 | 79.3 | 104 | 1 | WISMAT | alpha-amylase inhi |
| 123 | 23 | 79.3 | 119 | 2 | F65025 | hypothetical prote |
| 124 | 23 | 79.3 | 119 | 2 | E91048 | probable oxidoredu |
| 125 | 23 | 79.3 | 119 | 2 | A85893 | probable oxidoredu |
| 126 | 23 | 79.3 | 124 | 1 | GCAF | glucagon 1 precurs |
| 127 | 23 | 79.3 | 131 | 2 | S63742 | HIV-1 retropepsin |
| 128 | 23 | 79.3 | 136 | 2 | S63746 | HIV-1 retropepsin |
| 129 | 23 | 79.3 | 140 | 2 | S63737 | HIV-1 retropepsin |
| 130 | 23 | 79.3 | 141 | 2 | S63750 | HIV-1 retropepsin |

| | | | | | | |
|-----|----|------|-----|---|--------|---------------------|
| 131 | 23 | 79.3 | 142 | 2 | E72260 | iron-sulfur cofact |
| 132 | 23 | 79.3 | 146 | 2 | E95363 | protein [imported |
| 133 | 23 | 79.3 | 151 | 2 | S63748 | HIV-1 retropepsin |
| 134 | 23 | 79.3 | 151 | 2 | S63731 | HIV-1 retropepsin |
| 135 | 23 | 79.3 | 162 | 2 | S63732 | HIV-1 retropepsin |
| 136 | 23 | 79.3 | 196 | 2 | AG2803 | hypothetical prote |
| 137 | 23 | 79.3 | 196 | 2 | G97582 | hypothetical prote |
| 138 | 23 | 79.3 | 207 | 2 | E64718 | conserved hypothet |
| 139 | 23 | 79.3 | 225 | 2 | B84289 | hypothetical prote |
| 140 | 23 | 79.3 | 231 | 2 | H64466 | hypothetical prote |
| 141 | 23 | 79.3 | 249 | 2 | D85693 | unknown protein en |
| 142 | 23 | 79.3 | 260 | 2 | E70578 | probable wag31 pro |
| 143 | 23 | 79.3 | 265 | 2 | B96993 | probable membrane |
| 144 | 23 | 79.3 | 266 | 2 | T26068 | hypothetical prote |
| 145 | 23 | 79.3 | 267 | 2 | H97299 | proB [imported] - |
| 146 | 23 | 79.3 | 271 | 2 | E84138 | biotin synthesis B |
| 147 | 23 | 79.3 | 274 | 2 | T18768 | hypothetical prote |
| 148 | 23 | 79.3 | 275 | 2 | D81947 | probable amino aci |
| 149 | 23 | 79.3 | 275 | 2 | H81158 | amino acid ABC tra |
| 150 | 23 | 79.3 | 283 | 2 | T05727 | nucleic acid-bindin |

ALIGNMENTS

RESULT 1

T19354

hypothetical protein C17E4.10 - *Caenorhabditis elegans*

C;Species: *Caenorhabditis elegans*

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004.

C;Accession: T19354

R;Percy, C.

submitted to the EMBL Data Library, October 1996

A;Reference number: Z19113

A;Accession: T19354

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-386

A;Cross-references: UNIPROT:Q93231; UNIPARC:UPI0000163FFD; EMBL:Z81037; PIDN:CAB02748.

A;Experimental source: clone C17E4

C;Genetics:

A;Gene: CESP:C17E4.10

A;Map position: 1

A;Introns: 36/3; 98/2; 264/3; 309/2

Query Match 96.6%; Score 28; DB 2; Length 386;
 Best Local Similarity 75.0%; Pred. No. 17;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ADXTIXEE 8
 || || ||
 Db 134 ADTTIREE 141

RESULT 2

AI2108

hypothetical protein all2424 [imported] - *Nostoc* sp. (strain PCC 7120)

C;Species: *Nostoc* sp. PCC 7120

A;Note: *Nostoc* sp. strain PCC 7120 is a synonym of *Anabaena* sp. strain PCC 7120

C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004

C;Accession: AI2108

SCORE Search Results Details for Application 10763712 and Search Result us-10-763-712b-186.rnpbn.

| | | | | |
|----------------------------|--------------------------------------|------------------------------|-----------------------|-----------------------------|
| Score Home | Retrieve Application | SCORE System | SCORE | Comments / |
| Page | List | Overview | FAQ | Suggestions |

This page gives you Search Results detail for the Application 10763712 and Search Result us-10-763-712b-186.rnpbn.

[start](#)

[Go Back to previous](#)

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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 29, 2006, 20:17:32 ; Search time 55.6667 Seconds
(without alignments)
254.909 Million cell updates/sec

Title: US-10-763-712B-186
Perfect score: 29
Sequence: 1 ADXTIXEE 8

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 809770 seqs, 591248006 residues

Total number of hits satisfying chosen parameters: 1619540

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries

Command line parameters:

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-MODEL=frame+_p2n.model -DEV=xlh
-Q=/abss/ABSSWEB_spool/US10763712/runat_29062006_075109_19603/app_query.fasta_1
-DB=Published_Applications_NA_New -QFMT=fastap -SUFFIX=rnpbn -MINMATCH=0.1
-LOOPCL=0 -LOOEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=150 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=25 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -HOST=abss03h
-USER=US10763712 @CGN_1_1_154 @runat_29062006_075109_19603 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Database : Published_Applications_NA_New:*

1: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US09_NEW_PUB.seq:*
 2: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US06_NEW_PUB.seq:*
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 4: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US08_NEW_PUB.seq:*
 5: /EMC_Celerra_SIDS3/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
 6: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US10_NEW_PUB.seq:*
 7: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq:*
 8: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result | % | | Query | | | | Description |
|--------|-----|-------|-------|--------|-----------------------|-----------------------|-----------------------|
| | No. | Score | Match | Length | DB | ID | |
| c | 1 | 28 | 96.6 | 3566 | 6 | US-10-449-902-14853 | Sequence 14853, A |
| | 2 | 28 | 96.6 | 3807 | 6 | US-10-449-902-18976 | Sequence 18976, A |
| | 3 | 28 | 96.6 | 6707 | 7 | US-11-266-748A-32492 | Sequence 32492, A |
| c | 4 | 28 | 96.6 | 909203 | 7 | US-11-266-748A-29039 | Sequence 29039, A |
| c | 5 | 27 | 93.1 | 369 | 7 | US-11-266-748A-371617 | Sequence 371617, |
| | 6 | 27 | 93.1 | 369 | 7 | US-11-266-748A-454996 | Sequence 454996, |
| | 7 | 27 | 93.1 | 675 | 7 | US-11-217-529-5071 | Sequence 5071, Ap |
| c | 8 | 27 | 93.1 | 12783 | 7 | US-11-266-748A-31917 | Sequence 31917, A |
| | 9 | 27 | 93.1 | 13509 | 7 | US-11-266-748A-29788 | Sequence 29788, A |
| | 10 | 26 | 89.7 | 789 | 7 | US-11-251-208-291 | Sequence 291, App |
| | 11 | 26 | 89.7 | 1007 | 7 | US-11-266-748A-254215 | Sequence 254215, |
| | 12 | 26 | 89.7 | 1007 | 7 | US-11-266-748A-276868 | Sequence 276868, |
| | 13 | 26 | 89.7 | 1007 | 7 | US-11-266-748A-314732 | Sequence 314732, |
| | 14 | 26 | 89.7 | 1062 | 7 | US-11-216-545-8455 | Sequence 8455, Ap |
| | 15 | 26 | 89.7 | 1298 | 7 | US-11-216-545-8456 | Sequence 8456, Ap |
| | 16 | 26 | 89.7 | 3068 | 7 | US-11-238-155-51 | Sequence 51, Appl |
| | 17 | 26 | 89.7 | 3080 | 7 | US-11-238-155-52 | Sequence 52, Appl |
| | 18 | 26 | 89.7 | 3083 | 7 | US-11-238-155-61 | Sequence 61, Appl |
| | 19 | 26 | 89.7 | 3479 | 7 | US-11-238-155-5 | Sequence 5, Appli |
| | 20 | 26 | 89.7 | 12225 | 7 | US-11-238-155-1 | Sequence 1, Appli |
| | 21 | 25 | 86.2 | 520 | 6 | US-10-488-619-2681 | Sequence 2681, Ap |
| | 22 | 25 | 86.2 | 657 | 7 | US-11-266-748A-80468 | Sequence 80468, A |
| | 23 | 25 | 86.2 | 657 | 7 | US-11-266-748A-133279 | Sequence 133279, |
| | c | 24 | 25 | 86.2 | 1000 | 7 | US-11-266-748A-209252 |
| c | 25 | 25 | 86.2 | 1000 | 7 | US-11-266-748A-223970 | Sequence 223970, |
| 26 | 25 | 86.2 | 1070 | 6 | US-10-449-902-10908 | Sequence 10908, A | |
| c | 27 | 25 | 86.2 | 1546 | 7 | US-11-266-748A-57739 | Sequence 57739, A |
| c | 28 | 25 | 86.2 | 1918 | 7 | US-11-266-748A-356895 | Sequence 356895, |
| 29 | 25 | 86.2 | 1918 | 7 | US-11-266-748A-440274 | Sequence 440274, | |
| c | 30 | 25 | 86.2 | 2391 | 6 | US-10-449-902-27826 | Sequence 27826, A |
| 31 | 25 | 86.2 | 4614 | 7 | US-11-257-817-33 | Sequence 33, Appl | |
| 32 | 25 | 86.2 | 84323 | 7 | US-11-266-748A-61233 | Sequence 61233, A | |
| 33 | 24 | 82.8 | 306 | 7 | US-11-301-554-1544 | Sequence 1544, Ap | |
| 34 | 24 | 82.8 | 316 | 7 | US-11-301-554-285 | Sequence 285, App | |
| c | 35 | 24 | 82.8 | 438 | 7 | US-11-266-748A-169643 | Sequence 169643, |
| c | 36 | 24 | 82.8 | 481 | 7 | US-11-266-748A-5567 | Sequence 5567, Ap |
| 37 | 24 | 82.8 | 609 | 7 | US-11-266-748A-299490 | Sequence 299490, | |
| c | 38 | 24 | 82.8 | 614 | 6 | US-10-488-619-2891 | Sequence 2891, Ap |
| c | 39 | 24 | 82.8 | 840 | 6 | US-10-953-349-29706 | Sequence 29706, A |
| c | 40 | 24 | 82.8 | 1000 | 7 | US-11-266-748A-215119 | Sequence 215119, |
| c | 41 | 24 | 82.8 | 1000 | 7 | US-11-266-748A-216440 | Sequence 216440, |
| 42 | 24 | 82.8 | 1000 | 7 | US-11-266-748A-238248 | Sequence 238248, | |
| c | 43 | 24 | 82.8 | 1000 | 7 | US-11-266-748A-283914 | Sequence 283914, |

| | | | | | | | |
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| | 44 | 24 | 82.8 | 1000 | 7 | US-11-266-748A-335343 | Sequence 335343, |
| c | 45 | 24 | 82.8 | 1018 | 7 | US-11-266-748A-82029 | Sequence 82029, A |
| | 46 | 24 | 82.8 | 1018 | 7 | US-11-266-748A-134840 | Sequence 134840, |
| c | 47 | 24 | 82.8 | 1087 | 7 | US-11-266-748A-41880 | Sequence 41880, A |
| c | 48 | 24 | 82.8 | 1088 | 7 | US-11-266-748A-369681 | Sequence 369681, |
| | 49 | 24 | 82.8 | 1088 | 7 | US-11-266-748A-453060 | Sequence 453060, |
| c | 50 | 24 | 82.8 | 1090 | 7 | US-11-266-748A-353138 | Sequence 353138, |
| | 51 | 24 | 82.8 | 1090 | 7 | US-11-266-748A-436517 | Sequence 436517, |
| c | 52 | 24 | 82.8 | 1119 | 6 | US-10-449-902-16496 | Sequence 16496, A |
| c | 53 | 24 | 82.8 | 1133 | 7 | US-11-266-748A-91013 | Sequence 91013, A |
| | 54 | 24 | 82.8 | 1133 | 7 | US-11-266-748A-143824 | Sequence 143824, |
| c | 55 | 24 | 82.8 | 1136 | 6 | US-10-449-902-14735 | Sequence 14735, A |
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| | 64 | 24 | 82.8 | 1549 | 7 | US-11-266-748A-382037 | Sequence 382037, |
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| 143 | 23 | 79.3 | 732 | 7 | US-11-266-748A-98973 | Sequence 98973, A |
| c 144 | 23 | 79.3 | 732 | 7 | US-11-266-748A-151784 | Sequence 151784, |
| c 145 | 23 | 79.3 | 738 | 7 | US-11-266-748A-83427 | Sequence 83427, A |
| 146 | 23 | 79.3 | 738 | 7 | US-11-266-748A-136238 | Sequence 136238, |
| c 147 | 23 | 79.3 | 751 | 7 | US-11-266-748A-172520 | Sequence 172520, |
| c 148 | 23 | 79.3 | 752 | 7 | US-11-266-748A-179708 | Sequence 179708, |
| c 149 | 23 | 79.3 | 759 | 7 | US-11-266-748A-2226 | Sequence 2226, Ap |
| 150 | 23 | 79.3 | 759 | 7 | US-11-266-748A-62933 | Sequence 62933, A |

ALIGNMENTS

RESULT 1

US-10-449-902-14853

; Sequence 14853, Application US/10449902

; Publication No. US20060123505A1

; GENERAL INFORMATION:

; APPLICANT: National Institute of Agrobiological Sciences.

; APPLICANT: Bio-oriented Technology Research Advancement Institution.

; APPLICANT: The Institute of Physical and Chemical Research.

; APPLICANT: Foundation for Advancement of International Science.

; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF

; FILE REFERENCE: MOA-A0205Y1-US

SCORE Search Results Details for Application 10763712 and Search Result us-10-763-712b-186.rnpbm.

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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 29, 2006, 20:16:21 ; Search time 602.667 Seconds
(without alignments)
244.665 Million cell updates/sec

Title: US-10-763-712B-186
Perfect score: 29
Sequence: 1 ADXTIXEE 8

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries

Command line parameters:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 4 | 28 | 96.6 | 5323 | 8 | US-10-302-172-726 | Sequence 726, App |
| c 5 | 28 | 96.6 | 519599 | 10 | US-10-737-082-73 | Sequence 73, Appl |
| c 6 | 28 | 96.6 | 519599 | 10 | US-10-765-790-73 | Sequence 73, Appl |
| 7 | 28 | 96.6 | 608916 | 10 | US-10-461-862-1 | Sequence 1, Appli |
| 8 | 27 | 93.1 | 345 | 8 | US-10-424-599-126892 | Sequence 126892, |
| 9 | 27 | 93.1 | 514 | 3 | US-09-814-353-15867 | Sequence 15867, A |
| c 10 | 27 | 93.1 | 529 | 8 | US-10-767-701-26330 | Sequence 26330, A |
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| 18 | 27 | 93.1 | 1170 | 9 | US-10-411-910A-120 | Sequence 120, App |
| 19 | 27 | 93.1 | 1170 | 9 | US-10-411-910A-227 | Sequence 227, App |
| 20 | 27 | 93.1 | 1212 | 9 | US-10-411-910A-115 | Sequence 115, App |
| 21 | 27 | 93.1 | 1212 | 9 | US-10-411-910A-222 | Sequence 222, App |
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| 37 | 27 | 93.1 | 1368 | 9 | US-10-411-910A-240 | Sequence 240, App |
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| 59 | 27 | 93.1 | 1725 | 9 | US-10-411-910A-89 | Sequence 89, Appl |
| 60 | 27 | 93.1 | 1725 | 9 | US-10-411-910A-94 | Sequence 94, Appl |
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| 71 | 27 | 93.1 | 1749 | 9 | US-10-411-910A-218 | Sequence 218, App |
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| 80 | 27 | 93.1 | 1911 | 9 | US-10-411-910A-225 | Sequence 225, App |
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| 82 | 27 | 93.1 | 1935 | 9 | US-10-411-910A-232 | Sequence 232, App |
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ALIGNMENTS

RESULT 1

US-11-097-143-6821

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(without alignments)
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ALIGNMENTS

RESULT 1

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; Patent No. 6783969

; GENERAL INFORMATION:

; APPLICANT: Tang, Y. Tom

; APPLICANT: Zhou, Ping

; APPLICANT: Goodrich, Ryle

; APPLICANT: Asundi, Vinod

; APPLICANT: Ren, Feiyan

SCORE Search Results Details for Application 10 and Search Result us-10-763-712b-186.rn

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This page gives you Search Results detail for the Application 10763712 and Search Result us-10-763-712b-186.rn

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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 29, 2006, 19:28:24 ; Search time 264.667 Seconds
(without alignments)
316.122 Million cell updates/sec

Title: US-10-763-712B-186
Perfect score: 29
Sequence: 1 ADXTIXEE 8

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries

Command line parameters:

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-MODEL=frame+ p2n.model -DEV=xlh
-Q=/abss/ABSSWEB_spool/US10763712/runat_29062006_075054_19188/app_query.fasta_1
-DB=N_Geneseq -QFMT=fastap -SUFFIX=rng -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=150
-DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=25 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss07
-USER=US10763712 @CGN_1_1_942 @runat_29062006_075054_19188 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
```

Database : N_Geneseq_8:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*

5: geneseqn2001bs:*
 6: geneseqn2002as:*
 7: geneseqn2002bs:*
 8: geneseqn2003as:*
 9: geneseqn2003bs:*
 10: geneseqn2003cs:*
 11: geneseqn2003ds:*
 12: geneseqn2004as:*
 13: geneseqn2004bs:*
 14: geneseqn2005s:*
 15: geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result | No. | Score | % Query Match | Length | DB | ID | Description |
|--------|-----|-------|------------------|--------|----|------------|--------------------|
| | 1 | 29 | 100.0 | 1619 | 4 | ABL06387 | Abl06387 Drosophil |
| c | 2 | 29 | 100.0 | 6664 | 4 | ABL06386 | Abl06386 Drosophil |
| c | 3 | 28 | 96.6 | 3519 | 10 | ADD48568 | Add48568 Rat gene |
| | 4 | 28 | 96.6 | 4573 | 6 | ABZ11844 | Abz11844 Human pol |
| | 5 | 28 | 96.6 | 5264 | 10 | ACC72807 | Acc72807 Human can |
| | 6 | 28 | 96.6 | 5323 | 12 | ADM44362 | Adm44362 Novel hum |
| | 7 | 28 | 96.6 | 110000 | 13 | ABD32804_4 | Continuation (5 of |
| c | 8 | 28 | 96.6 | 110000 | 14 | AEA61163_3 | Continuation (4 of |
| | 9 | 27 | 93.1 | 178 | 13 | ADT91309 | Adt91309 Chlamydom |
| | 10 | 27 | 93.1 | 178 | 13 | ADT91311 | Adt91311 Clostridi |
| | 11 | 27 | 93.1 | 178 | 13 | ADT91308 | Adt91308 Clostridi |
| | 12 | 27 | 93.1 | 178 | 13 | ADT91312 | Adt91312 Chlamydom |
| | 13 | 27 | 93.1 | 391 | 3 | AAA41815 | Aaa41815 Human sec |
| | 14 | 27 | 93.1 | 514 | 5 | ADL41977 | Adl41977 Human ova |
| | 15 | 27 | 93.1 | 909 | 10 | ADF18737 | Adf18737 DNA-depen |
| | 16 | 27 | 93.1 | 1048 | 5 | AAH51931 | Aah51931 HIV prote |
| | 17 | 27 | 93.1 | 1048 | 12 | ADH44796 | Adh44796 HIV prote |
| | 18 | 27 | 93.1 | 1164 | 10 | ADF18738 | Adf18738 DNA-depen |
| | 19 | 27 | 93.1 | 1311 | 14 | AEB73392 | Aeb73392 DNA encod |
| | 20 | 27 | 93.1 | 1350 | 14 | AEB73391 | Aeb73391 DNA encod |
| | 21 | 27 | 93.1 | 1494 | 14 | AEB73387 | Aeb73387 cDNA enco |
| | 22 | 27 | 93.1 | 1544 | 14 | ADZ39228 | Adz39228 Trichomon |
| | 23 | 27 | 93.1 | 1725 | 14 | AEB73388 | Aeb73388 cDNA enco |
| | 24 | 27 | 93.1 | 1737 | 2 | AAZ25198 | Aaz25198 Clostridi |
| | 25 | 27 | 93.1 | 1737 | 2 | AAZ25199 | Aaz25199 Clostridi |
| | 26 | 27 | 93.1 | 1740 | 8 | ACA28640 | Aca28640 Prokaryot |
| | 27 | 27 | 93.1 | 1749 | 8 | ACA27971 | Aca27971 Prokaryot |
| | 28 | 27 | 93.1 | 1900 | 2 | AAZ25197 | Aaz25197 Nucleotid |
| | 29 | 27 | 93.1 | 2244 | 8 | ACA45756 | Aca45756 Prokaryot |
| | 30 | 27 | 93.1 | 2347 | 10 | ADC59543 | Adc59543 Clostridi |
| | 31 | 27 | 93.1 | 2347 | 13 | ADR90306 | Adr90306 Clostridi |
| | 32 | 27 | 93.1 | 2399 | 14 | ADY27752 | Ady27752 Chlamydom |
| | 33 | 27 | 93.1 | 2421 | 14 | ADY27753 | Ady27753 Chlorella |
| | 34 | 27 | 93.1 | 2463 | 10 | ADF18739 | Adf18739 DNA-depen |
| | 35 | 27 | 93.1 | 2566 | 4 | AAF74655 | Aaf74655 Mouse int |
| | 36 | 27 | 93.1 | 2636 | 14 | ADY27751 | Ady27751 Scenedesm |
| | 37 | 27 | 93.1 | 3265 | 14 | ADY27747 | Ady27747 Chlorella |
| | 38 | 27 | 93.1 | 3340 | 14 | ADZ74219 | Adz74219 Corynebac |
| c | 39 | 27 | 93.1 | 4410 | 10 | ADB69953 | Adb69953 C. neofo |
| | 40 | 27 | 93.1 | 5001 | 14 | ADY27745 | Ady27745 Scenedesm |

| | | | | | | | |
|-----|----|------|------|-------|----------|--------------------|--------------------|
| c | 41 | 27 | 93.1 | 5172 | 10 | ADB69592 | Adb69592 C. neofor |
| | 42 | 27 | 93.1 | 5200 | 14 | ADY27766 | Ady27766 Chlamydom |
| | 43 | 27 | 93.1 | 5208 | 14 | ADY27746 | Ady27746 Chlamydom |
| c | 44 | 27 | 93.1 | 6826 | 10 | ADB69231 | Adb69231 C. neofor |
| | 45 | 27 | 93.1 | 12387 | 12 | ADJ62733 | Adj62733 Human cDN |
| | 46 | 27 | 93.1 | 12780 | 2 | AAX04535 | Aax04535 DNA encod |
| | 47 | 27 | 93.1 | 12780 | 8 | ACC49402 | Acc49402 Human DNA |
| | 48 | 27 | 93.1 | 12783 | 10 | ADD14669 | Add14669 Human src |
| | 49 | 27 | 93.1 | 13375 | 6 | ABQ93457 | Abq93457 Human cDN |
| | 50 | 27 | 93.1 | 13468 | 6 | ABQ93458 | Abq93458 Human cDN |
| | 51 | 27 | 93.1 | 13509 | 8 | ABX76175 | Abx76175 Lung canc |
| | 52 | 27 | 93.1 | 13509 | 10 | ADE85658 | Ade85658 Farnesyl |
| | 53 | 27 | 93.1 | 13509 | 10 | ADF18734 | Adf18734 DNA-depen |
| | 54 | 27 | 93.1 | 13509 | 14 | ADX05477 | Adx05477 Cyclin-de |
| | 55 | 27 | 93.1 | 13509 | 15 | AEF74615 | Aef74615 Human pol |
| | 56 | 27 | 93.1 | 13509 | 15 | AEF75056 | Aef75056 Human pol |
| | 57 | 26 | 89.7 | 30 | 3 | AAZ97998 | Aaz97998 HIV-1 pro |
| | 58 | 26 | 89.7 | 51 | 6 | ABA01273 | Aba01273 Pseudokno |
| | 59 | 26 | 89.7 | 54 | 3 | AAA40249 | Aaa40249 HIV-1 iso |
| c | 60 | 26 | 89.7 | 84 | 2 | AAV57198 | Aav57198 Oligonucl |
| c | 61 | 26 | 89.7 | 84 | 10 | ADD54950 | Add54950 Walk thro |
| | 62 | 26 | 89.7 | 90 | 15 | AEF88398 | Aef88398 HIV-1 gag |
| | 63 | 26 | 89.7 | 279 | 2 | AAQ30211 | Aaq30211 HIV-DASH |
| | 64 | 26 | 89.7 | 297 | 2 | AAQ34788 | Aaq34788 Synthetic |
| | 65 | 26 | 89.7 | 297 | 2 | AAT67281 | Aat67281 HIV-1 pro |
| | 66 | 26 | 89.7 | 297 | 6 | ABL39987 | Abl39987 Synthetic |
| | 67 | 26 | 89.7 | 297 | 6 | ABL39988 | Abl39988 Wild type |
| | 68 | 26 | 89.7 | 297 | 6 | ABL39985 | Abl39985 Synthetic |
| | 69 | 26 | 89.7 | 297 | 6 | ABL39986 | Abl39986 Wild type |
| | 70 | 26 | 89.7 | 297 | 6 | ABA01911 | Aba01911 Human imm |
| | 71 | 26 | 89.7 | 297 | 6 | ABA01910 | Aba01910 Human imm |
| | 72 | 26 | 89.7 | 297 | 8 | ACA03555 | Aca03555 Synthetic |
| | 73 | 26 | 89.7 | 297 | 8 | ACA03556 | Aca03556 Synthetic |
| | 74 | 26 | 89.7 | 297 | 8 | ACC78512 | Acc78512 HIV protI |
| | 75 | 26 | 89.7 | 297 | 8 | ACC78511 | Acc78511 HIV prot. |
| | 76 | 26 | 89.7 | 297 | 10 | ADC73264 | Adc73264 NL4-3 Hum |
| | 77 | 26 | 89.7 | 297 | 10 | ADE29179 | Ade29179 HIV-1 PR |
| | 78 | 26 | 89.7 | 297 | 12 | ADH56295 | Adh56295 HIV NL4-3 |
| | 79 | 26 | 89.7 | 297 | 12 | ADH67954 | Adh67954 Human imm |
| | 80 | 26 | 89.7 | 297 | 12 | ADM73798 | Adm73798 HIV-1 pol |
| | 81 | 26 | 89.7 | 297 | 12 | ADM73800 | Adm73800 HIV-1 pol |
| | 82 | 26 | 89.7 | 297 | 12 | ADM73799 | Adm73799 HIV-1 pol |
| | 83 | 26 | 89.7 | 297 | 12 | ADM73801 | Adm73801 HIV-1 pol |
| | 84 | 26 | 89.7 | 297 | 15 | AEF07077 | Aef07077 HIV-1 sub |
| | 85 | 26 | 89.7 | 297 | 15 | AEF07073 | Aef07073 HIV-1 sub |
| | 86 | 26 | 89.7 | 303 | 10 | ADL18135 | Adl18135 HIV-1 pro |
| | 87 | 26 | 89.7 | 329 | 4 | AAF28778 | Aaf28778 HIV trans |
| | 88 | 26 | 89.7 | 339 | 2 | AAQ72414 | Aaq72414 NY5 strai |
| | 89 | 26 | 89.7 | 375 | 2 | AAQ05116 | Aaq05116 HIV-1 pro |
| | 90 | 26 | 89.7 | 375 | 2 | AAQ73660 | Aaq73660 HIV-1 BH1 |
| | 91 | 26 | 89.7 | 402 | 2 | AAQ05114 | Aaq05114 HIV-1 pro |
| | 92 | 26 | 89.7 | 477 | 1 | AAN70427 | Aan70427 The DNA s |
| | 93 | 26 | 89.7 | 507 | 10 | ADB87785 | Adb87785 HIV-1 BH1 |
| | 94 | 26 | 89.7 | 507 | 10 | ADD66307 | Add66307 HIV-1 pro |
| | 95 | 26 | 89.7 | 507 | 12 | ADI05580 | Adi05580 Novel ade |
| | 96 | 26 | 89.7 | 507 | 13 | ADS82142 | Ads82142 DNA seque |
| | 97 | 26 | 89.7 | 535 | 2 | AAQ05115 | Aaq05115 HIV-1 pro |
| | 98 | 26 | 89.7 | 627 | 6 | ABK78196 | Abk78196 Bacillus |
| | 99 | 26 | 89.7 | 630 | 2 | AAQ11713 | Aaq11713 Sequence |
| 100 | 26 | 89.7 | 630 | 2 | AAQ50157 | Aaq50157 Gag and p | |
| 101 | 26 | 89.7 | 660 | 2 | AAZ21351 | Aaz21351 Recombina | |

| | | | | | | |
|-------|----|------|------|----|----------|--------------------|
| 102 | 26 | 89.7 | 751 | 6 | ABK73718 | Abk73718 Bacillus |
| 103 | 26 | 89.7 | 789 | 13 | ADT87706 | Adt87706 Plant cDN |
| c 104 | 26 | 89.7 | 798 | 13 | ADS58725 | Ads58725 Bacterial |
| 105 | 26 | 89.7 | 885 | 8 | ACA22181 | Aca22181 Prokaryot |
| 106 | 26 | 89.7 | 898 | 8 | ACA22453 | Aca22453 Prokaryot |
| 107 | 26 | 89.7 | 1009 | 11 | ACN90366 | Acn90366 Breast ca |
| c 108 | 26 | 89.7 | 1040 | 5 | AAH80073 | Aah80073 HIV PRT a |
| c 109 | 26 | 89.7 | 1040 | 10 | ADD80964 | Add80964 HIV PRT a |
| c 110 | 26 | 89.7 | 1040 | 14 | ADW99666 | Adw99666 HIV PRT D |
| 111 | 26 | 89.7 | 1045 | 5 | AAH51832 | Aah51832 HIV prote |
| 112 | 26 | 89.7 | 1045 | 12 | ADH44697 | Adh44697 HIV prote |
| 113 | 26 | 89.7 | 1046 | 5 | AAH51833 | Aah51833 HIV prote |
| 114 | 26 | 89.7 | 1046 | 12 | ADH44698 | Adh44698 HIV prote |
| 115 | 26 | 89.7 | 1053 | 5 | AAH51871 | Aah51871 HIV prote |
| 116 | 26 | 89.7 | 1053 | 12 | ADH44736 | Adh44736 HIV prote |
| 117 | 26 | 89.7 | 1059 | 5 | AAH51870 | Aah51870 HIV prote |
| 118 | 26 | 89.7 | 1059 | 12 | ADH44735 | Adh44735 HIV prote |
| 119 | 26 | 89.7 | 1082 | 5 | AAH51872 | Aah51872 HIV prote |
| 120 | 26 | 89.7 | 1082 | 12 | ADH44737 | Adh44737 HIV prote |
| 121 | 26 | 89.7 | 1113 | 5 | AAH51856 | Aah51856 HIV prote |
| 122 | 26 | 89.7 | 1113 | 12 | ADH44721 | Adh44721 HIV prote |
| 123 | 26 | 89.7 | 1115 | 5 | AAH51920 | Aah51920 HIV prote |
| 124 | 26 | 89.7 | 1115 | 5 | AAH51928 | Aah51928 HIV prote |
| 125 | 26 | 89.7 | 1115 | 5 | AAH51927 | Aah51927 HIV prote |
| 126 | 26 | 89.7 | 1115 | 12 | ADH44785 | Adh44785 HIV prote |
| 127 | 26 | 89.7 | 1115 | 12 | ADH44793 | Adh44793 HIV prote |
| 128 | 26 | 89.7 | 1115 | 12 | ADH44792 | Adh44792 HIV prote |
| 129 | 26 | 89.7 | 1116 | 5 | AAH51843 | Aah51843 HIV prote |
| 130 | 26 | 89.7 | 1116 | 5 | AAH51873 | Aah51873 HIV prote |
| 131 | 26 | 89.7 | 1116 | 5 | AAH51880 | Aah51880 HIV prote |
| 132 | 26 | 89.7 | 1116 | 5 | AAH51944 | Aah51944 HIV prote |
| 133 | 26 | 89.7 | 1116 | 5 | AAH51840 | Aah51840 HIV prote |
| 134 | 26 | 89.7 | 1116 | 5 | AAH51858 | Aah51858 HIV prote |
| 135 | 26 | 89.7 | 1116 | 5 | AAH51932 | Aah51932 HIV prote |
| 136 | 26 | 89.7 | 1116 | 5 | AAH51939 | Aah51939 HIV prote |
| 137 | 26 | 89.7 | 1116 | 5 | AAH51857 | Aah51857 HIV prote |
| 138 | 26 | 89.7 | 1116 | 5 | AAH51865 | Aah51865 HIV prote |
| 139 | 26 | 89.7 | 1116 | 5 | AAH51878 | Aah51878 HIV prote |
| 140 | 26 | 89.7 | 1116 | 5 | AAH51885 | Aah51885 HIV prote |
| 141 | 26 | 89.7 | 1116 | 5 | AAH51886 | Aah51886 HIV prote |
| 142 | 26 | 89.7 | 1116 | 5 | AAH51914 | Aah51914 HIV prote |
| 143 | 26 | 89.7 | 1116 | 5 | AAH51915 | Aah51915 HIV prote |
| 144 | 26 | 89.7 | 1116 | 5 | AAH51924 | Aah51924 HIV prote |
| 145 | 26 | 89.7 | 1116 | 5 | AAH51942 | Aah51942 HIV prote |
| 146 | 26 | 89.7 | 1116 | 5 | AAH51884 | Aah51884 HIV prote |
| 147 | 26 | 89.7 | 1116 | 5 | AAH51891 | Aah51891 HIV prote |
| 148 | 26 | 89.7 | 1116 | 5 | AAH51922 | Aah51922 HIV prote |
| 149 | 26 | 89.7 | 1116 | 5 | AAH51923 | Aah51923 HIV prote |
| 150 | 26 | 89.7 | 1116 | 5 | AAH51881 | Aah51881 HIV prote |

ALIGNMENTS

RESULT 1

ABL06387

ID ABL06387 standard; cDNA; 1619 BP.

XX

AC ABL06387;

XX

DT 26-MAR-2002 (first entry)

XX

SCORE Search Results Details for Application 10763712 and Search Result us-10-763-712b-186.rapbn.

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|----------------------------|--------------------------------------|------------------------------|-----------------------|-----------------------------|
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OM protein - protein search, using sw model

Run on: June 29, 2006, 08:32:53 ; Search time 8 Seconds
(without alignments)
23.620 Million cell updates/sec

Title: US-10-763-712B-186
Perfect score: 29
Sequence: 1 ADXTIXEE 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 103426 seqs, 23619683 residues

Total number of hits satisfying chosen parameters: 103426

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries

Database : Published Applications_AA New:*

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- 2: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
- 3: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
- 4: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
- 5: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
- 6: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
- 7: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
- 8: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| | |
|--------|------------|
| Result | % Query |
|--------|------------|

| No. | Score | Match Length | DB | ID | Description |
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| 1 | 26 | 89.7 | 262 | 7 | US-11-251-208-292 |
| 2 | 25 | 86.2 | 205 | 6 | US-10-449-902-39360 |
| 3 | 24 | 82.8 | 213 | 6 | US-10-953-349-4970 |
| 4 | 24 | 82.8 | 223 | 6 | US-10-953-349-4969 |
| 5 | 24 | 82.8 | 290 | 6 | US-10-953-349-4968 |
| 6 | 24 | 82.8 | 479 | 6 | US-10-449-902-55806 |
| 7 | 24 | 82.8 | 684 | 6 | US-10-471-571A-3984 |
| 8 | 24 | 82.8 | 687 | 6 | US-10-449-902-55507 |
| 9 | 23 | 79.3 | 124 | 6 | US-10-953-349-25565 |
| 10 | 23 | 79.3 | 153 | 6 | US-10-953-349-25564 |
| 11 | 23 | 79.3 | 177 | 6 | US-10-449-902-35915 |
| 12 | 23 | 79.3 | 185 | 6 | US-10-953-349-25898 |
| 13 | 23 | 79.3 | 257 | 6 | US-10-449-902-33412 |
| 14 | 23 | 79.3 | 261 | 7 | US-11-251-208-375 |
| 15 | 23 | 79.3 | 262 | 7 | US-11-251-208-327 |
| 16 | 23 | 79.3 | 278 | 6 | US-10-953-349-21727 |
| 17 | 23 | 79.3 | 278 | 6 | US-10-953-349-30328 |
| 18 | 23 | 79.3 | 283 | 6 | US-10-953-349-21726 |
| 19 | 23 | 79.3 | 283 | 6 | US-10-953-349-30327 |
| 20 | 23 | 79.3 | 296 | 6 | US-10-196-749-32 |
| 21 | 23 | 79.3 | 300 | 6 | US-10-953-349-21725 |
| 22 | 23 | 79.3 | 300 | 6 | US-10-953-349-30326 |
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| 24 | 23 | 79.3 | 339 | 6 | US-10-449-902-36091 |
| 25 | 23 | 79.3 | 358 | 6 | US-10-449-902-47148 |
| 26 | 23 | 79.3 | 396 | 6 | US-10-449-902-39764 |
| 27 | 23 | 79.3 | 472 | 7 | US-11-283-329-50 |
| 28 | 23 | 79.3 | 505 | 6 | US-10-449-902-44195 |
| 29 | 23 | 79.3 | 556 | 6 | US-10-449-902-35255 |
| 30 | 23 | 79.3 | 564 | 6 | US-10-449-902-42720 |
| 31 | 23 | 79.3 | 569 | 6 | US-10-449-902-36745 |
| 32 | 23 | 79.3 | 647 | 6 | US-10-449-902-40030 |
| 33 | 23 | 79.3 | 774 | 6 | US-10-953-349-38348 |
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| 35 | 23 | 79.3 | 793 | 6 | US-10-953-349-38346 |
| 36 | 23 | 79.3 | 808 | 6 | US-10-449-902-41350 |
| 37 | 23 | 79.3 | 821 | 6 | US-10-449-902-41595 |
| 38 | 23 | 79.3 | 884 | 6 | US-10-449-902-41592 |
| 39 | 23 | 79.3 | 996 | 6 | US-10-449-902-41122 |
| 40 | 23 | 79.3 | 1108 | 6 | US-10-449-902-42926 |
| 41 | 23 | 79.3 | 1125 | 6 | US-10-449-902-46131 |
| 42 | 23 | 79.3 | 1379 | 6 | US-10-449-902-41269 |
| 43 | 23 | 79.3 | 1674 | 6 | US-10-511-937-2587 |
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| 45 | 22 | 75.9 | 142 | 6 | US-10-449-902-50587 |
| 46 | 22 | 75.9 | 159 | 6 | US-10-953-349-2808 |
| 47 | 22 | 75.9 | 160 | 6 | US-10-449-902-49029 |
| 48 | 22 | 75.9 | 165 | 6 | US-10-953-349-2807 |
| 49 | 22 | 75.9 | 172 | 7 | US-11-293-697-3637 |
| 50 | 22 | 75.9 | 194 | 6 | US-10-953-349-2806 |
| 51 | 22 | 75.9 | 292 | 6 | US-10-953-349-19090 |
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| 53 | 22 | 75.9 | 299 | 6 | US-10-953-349-19089 |
| 54 | 22 | 75.9 | 301 | 6 | US-10-449-902-30780 |
| 55 | 22 | 75.9 | 310 | 6 | US-10-953-349-19088 |
| 56 | 22 | 75.9 | 317 | 7 | US-11-121-154-71 |
| 57 | 22 | 75.9 | 319 | 6 | US-10-449-902-50840 |
| 58 | 22 | 75.9 | 319 | 6 | US-10-449-902-56791 |
| 59 | 22 | 75.9 | 373 | 6 | US-10-953-349-865 |

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| 60 | 22 | 75.9 | 373 | 7 | US-11-113-081A-2 | Sequence 2, Appli |
| 61 | 22 | 75.9 | 402 | 6 | US-10-449-902-31127 | Sequence 31127, A |
| 62 | 22 | 75.9 | 433 | 6 | US-10-471-571A-298 | Sequence 298, App |
| 63 | 22 | 75.9 | 475 | 7 | US-11-293-697-3563 | Sequence 3563, Ap |
| 64 | 22 | 75.9 | 509 | 6 | US-10-449-902-32749 | Sequence 32749, A |
| 65 | 22 | 75.9 | 520 | 6 | US-10-449-902-44765 | Sequence 44765, A |
| 66 | 22 | 75.9 | 521 | 6 | US-10-449-902-40577 | Sequence 40577, A |
| 67 | 22 | 75.9 | 572 | 6 | US-10-449-902-45447 | Sequence 45447, A |
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ALIGNMENTS

RESULT 1

US-11-251-208-292

; Sequence 292, Application US/11251208

; Publication No. US20060137043A1

; GENERAL INFORMATION:

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; APPLICANT: Sarria-Millan, Rodrigo

; APPLICANT: Mckersie, Bryan

; APPLICANT: Chen, Ruoying

; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES ENCODING PROTEINS ASSOCIATED WITH ABIOTI

; TITLE OF INVENTION: STRESS RESPONSE AND PLANT CELLS AND PLANTS WITH INCREASED

; TITLE OF INVENTION: TOLERANCE TO ENVIRONMENTAL STRESS

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; PRIOR APPLICATION NUMBER: EP 03016672.2

; PRIOR FILING DATE: 2003-08-01

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ALIGNMENTS

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US-10-813-977-34

; Sequence 34, Application US/10813977

; Publication No. US20050220796A1

; GENERAL INFORMATION:

; APPLICANT: Dynan, William

; APPLICANT: Takeda, Yoshihiko

; APPLICANT: Li, Shuyi

; TITLE OF INVENTION: Compositions and Methods for Modulating DNA Repair

; FILE REFERENCE: 791301-1010

; CURRENT APPLICATION NUMBER: US/10/813,977

; CURRENT FILING DATE: 2004-03-31

; NUMBER OF SEQ ID NOS: 36

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 34

; LENGTH: 25

; TYPE: PRT

; ORGANISM: Artificial

; FEATURE:

; OTHER INFORMATION: non-binding sequence

US-10-813-977-34

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US-10-077-699C-6

; Sequence 6, Application US/10077699C

; Patent No. 6858718

; GENERAL INFORMATION:

; APPLICANT: Happe, Thomas

; TITLE OF INVENTION: Hydrogen Production

; FILE REFERENCE: 01MEL1

; CURRENT APPLICATION NUMBER: US/10/077,699C

; CURRENT FILING DATE: 2002-02-15

; NUMBER OF SEQ ID NOS: 9

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 6

; LENGTH: 436

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; ORGANISM: Chlorella fusca

US-10-077-699C-6

Query Match 93.1%; Score 27; DB 2; Length 436;

Best Local Similarity 75.0%; Pred. No. 1.1e+02;

Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 105 ADLTIMEE 112

SCORE Search Results Details for Application 10763712 and Search Result us-10-763-712b- 186.rag.

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| 63 | 27 | 93.1 | 608 | 9 | AEB73230 | Aeb73230 | Segment o |
| 64 | 27 | 93.1 | 608 | 9 | AEB73304 | Aeb73304 | Segment o |
| 65 | 27 | 93.1 | 636 | 9 | AEB73243 | Aeb73243 | Segment o |
| 66 | 27 | 93.1 | 636 | 9 | AEB73307 | Aeb73307 | Segment o |
| 67 | 27 | 93.1 | 644 | 9 | AEB73250 | Aeb73250 | Segment o |
| 68 | 27 | 93.1 | 821 | 7 | ADF18727 | Adf18727 | DNA-depen |
| 69 | 27 | 93.1 | 844 | 9 | AEB73262 | Aeb73262 | Segment o |
| 70 | 27 | 93.1 | 1206 | 9 | AEB73232 | Aeb73232 | Segment o |
| 71 | 27 | 93.1 | 1206 | 9 | AEB73313 | Aeb73313 | Segment o |
| 72 | 27 | 93.1 | 4095 | 3 | AA49938 | Aay49938 | Human DNA |
| 73 | 27 | 93.1 | 4095 | 6 | ABU03906 | Abu03906 | Human exp |
| 74 | 27 | 93.1 | 4096 | 2 | AAW84272 | Aaw84272 | A DNA-dep |
| 75 | 27 | 93.1 | 4096 | 6 | ABP97121 | Abp97121 | Human DNA |
| 76 | 27 | 93.1 | 4096 | 6 | ABU03905 | Abu03905 | Human exp |
| 77 | 27 | 93.1 | 4097 | 5 | ABP62978 | Abp62978 | Human pol |
| 78 | 27 | 93.1 | 4097 | 6 | ABU03903 | Abu03903 | Human exp |
| 79 | 27 | 93.1 | 4097 | 7 | ADD14074 | Add14074 | Human src |
| 80 | 27 | 93.1 | 4097 | 7 | ADJ69792 | Adj69792 | Human hea |
| 81 | 27 | 93.1 | 4128 | 5 | ABP62979 | Abp62979 | Human pol |
| 82 | 27 | 93.1 | 4128 | 6 | ABU56454 | Abu56454 | Lung canc |
| 83 | 27 | 93.1 | 4128 | 6 | ABU03907 | Abu03907 | Human exp |
| 84 | 27 | 93.1 | 4128 | 6 | ABU03902 | Abu03902 | Human exp |
| 85 | 27 | 93.1 | 4128 | 6 | ABU03908 | Abu03908 | Human exp |
| 86 | 27 | 93.1 | 4128 | 7 | ADF18722 | Adf18722 | DNA-depen |
| 87 | 27 | 93.1 | 4128 | 8 | ADJ66486 | Adj66486 | DNA-depen |
| 88 | 27 | 93.1 | 4128 | 9 | ADX05478 | Adx05478 | Cyclin-de |
| 89 | 26 | 89.7 | 10 | 4 | ABP13545 | Abp13545 | HIV A02 s |
| 90 | 26 | 89.7 | 10 | 4 | ABP18128 | Abp18128 | HIV B58 s |
| 91 | 26 | 89.7 | 10 | 4 | ABP18057 | Abp18057 | HIV B58 s |
| 92 | 26 | 89.7 | 10 | 4 | ABP13546 | Abp13546 | HIV A02 s |
| 93 | 26 | 89.7 | 15 | 9 | ADV22394 | Adv22394 | HIV-1 Pol |
| 94 | 26 | 89.7 | 15 | 9 | ADV22393 | Adv22393 | HIV-1 Pol |
| 95 | 26 | 89.7 | 17 | 9 | ADV23802 | Adv23802 | HIV-1 pro |
| 96 | 26 | 89.7 | 23 | 6 | ABR55514 | Abr55514 | Amino aci |
| 97 | 26 | 89.7 | 23 | 6 | ABR55515 | Abr55515 | Protein p |
| 98 | 26 | 89.7 | 36 | 5 | AAU11473 | Aau11473 | Orthogona |
| 99 | 26 | 89.7 | 40 | 2 | AAW04520 | Aaw04520 | HIV-1 K41 |
| 100 | 26 | 89.7 | 40 | 2 | AAW04519 | Aaw04519 | HIV-1 K41 |
| 101 | 26 | 89.7 | 40 | 2 | AAW04517 | Aaw04517 | HIV-1 K41 |
| 102 | 26 | 89.7 | 99 | 1 | AAP81511 | Aap81511 | HIV-1 pro |
| 103 | 26 | 89.7 | 99 | 2 | AAR25641 | Aar25641 | HIV-1 AP |
| 104 | 26 | 89.7 | 99 | 2 | AAW04521 | Aaw04521 | HIV-1 K41 |
| 105 | 26 | 89.7 | 99 | 2 | AAW30563 | Aaw30563 | HIV-1 GAG |
| 106 | 26 | 89.7 | 99 | 2 | AAW30570 | Aaw30570 | HIV-1 gag |
| 107 | 26 | 89.7 | 99 | 2 | ABB09012 | Abb09012 | Protein # |
| 108 | 26 | 89.7 | 99 | 2 | ABB09011 | Abb09011 | Protein # |
| 109 | 26 | 89.7 | 99 | 2 | ABB09010 | Abb09010 | Protein # |
| 110 | 26 | 89.7 | 99 | 2 | AAU77768 | Aau77768 | Human imm |
| 111 | 26 | 89.7 | 99 | 2 | AAU77769 | Aau77769 | Human imm |
| 112 | 26 | 89.7 | 99 | 2 | AAU77770 | Aau77770 | Human imm |
| 113 | 26 | 89.7 | 99 | 2 | AAU77772 | Aau77772 | Human imm |
| 114 | 26 | 89.7 | 99 | 2 | AAU77767 | Aau77767 | Human imm |
| 115 | 26 | 89.7 | 99 | 2 | AAU77771 | Aau77771 | Human imm |
| 116 | 26 | 89.7 | 99 | 4 | AAB37117 | Aab37117 | HIV trans |
| 117 | 26 | 89.7 | 99 | 5 | AAU11489 | Aau11489 | HIV prote |
| 118 | 26 | 89.7 | 99 | 5 | AAM51911 | Aam51911 | Human imm |

| | | | | | | |
|-----|----|------|----|---|----------|--------------------|
| 119 | 26 | 89.7 | 99 | 5 | AAM51912 | Aam51912 Human imm |
| 120 | 26 | 89.7 | 99 | 7 | ADC73263 | Adc73263 NL4-3 Hum |
| 121 | 26 | 89.7 | 99 | 7 | ADE29024 | Ade29024 HIV-1 PR |
| 122 | 26 | 89.7 | 99 | 7 | ADE77498 | Ade77498 Protease |
| 123 | 26 | 89.7 | 99 | 7 | ADE77511 | Ade77511 Protease |
| 124 | 26 | 89.7 | 99 | 7 | ADE77502 | Ade77502 Protease |
| 125 | 26 | 89.7 | 99 | 7 | ADE77519 | Ade77519 Protease |
| 126 | 26 | 89.7 | 99 | 7 | ADE77560 | Ade77560 Protease |
| 127 | 26 | 89.7 | 99 | 7 | ADE77497 | Ade77497 Protease |
| 128 | 26 | 89.7 | 99 | 7 | ADE77499 | Ade77499 Protease |
| 129 | 26 | 89.7 | 99 | 7 | ADE77557 | Ade77557 Protease |
| 130 | 26 | 89.7 | 99 | 7 | ADE77526 | Ade77526 Protease |
| 131 | 26 | 89.7 | 99 | 7 | ADE77529 | Ade77529 Protease |
| 132 | 26 | 89.7 | 99 | 7 | ADE77537 | Ade77537 Protease |
| 133 | 26 | 89.7 | 99 | 7 | ADE77495 | Ade77495 HIV-1 pro |
| 134 | 26 | 89.7 | 99 | 7 | ADE77558 | Ade77558 Protease |
| 135 | 26 | 89.7 | 99 | 7 | ADE77527 | Ade77527 Protease |
| 136 | 26 | 89.7 | 99 | 7 | ADE77506 | Ade77506 Protease |
| 137 | 26 | 89.7 | 99 | 7 | ADE77513 | Ade77513 Protease |
| 138 | 26 | 89.7 | 99 | 7 | ADE77524 | Ade77524 Protease |
| 139 | 26 | 89.7 | 99 | 7 | ADE77559 | Ade77559 Protease |
| 140 | 26 | 89.7 | 99 | 7 | ADE77503 | Ade77503 Protease |
| 141 | 26 | 89.7 | 99 | 7 | ADE77518 | Ade77518 Protease |
| 142 | 26 | 89.7 | 99 | 7 | ADE77525 | Ade77525 Protease |
| 143 | 26 | 89.7 | 99 | 7 | ADE77512 | Ade77512 Protease |
| 144 | 26 | 89.7 | 99 | 7 | ADE77528 | Ade77528 Protease |
| 145 | 26 | 89.7 | 99 | 7 | ADE77496 | Ade77496 Protease |
| 146 | 26 | 89.7 | 99 | 7 | ADE77505 | Ade77505 Protease |
| 147 | 26 | 89.7 | 99 | 7 | ADE77520 | Ade77520 Protease |
| 148 | 26 | 89.7 | 99 | 7 | ADE77501 | Ade77501 Protease |
| 149 | 26 | 89.7 | 99 | 7 | ADE77545 | Ade77545 Protease |
| 150 | 26 | 89.7 | 99 | 7 | ADE77500 | Ade77500 Protease |

ALIGNMENTS

RESULT 1

ABR58656

ID ABR58656 standard; protein; 1482 AA.

XX

AC ABR58656;

XX

DT 09-JUL-2003 (first entry)

XX

DE Human cancer related protein SEQ ID NO:313.

XX

KW Human; cancer; diagnosis; screening; modulator; leukaemia; ischaemia;

KW heart disease; atherosclerosis; endometriosis.

XX

OS Homo sapiens.

XX

PN WO2003025138-A2.

XX

PD 27-MAR-2003.

XX

PF 17-SEP-2002; 2002WO-US029560.

XX

PR 17-SEP-2001; 2001US-0323469P.

PR 20-SEP-2001; 2001US-0323887P.

PR 13-NOV-2001; 2001US-0350666P.

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OM protein - protein search, using sw model

Run on: June 29, 2006, 08:19:13 ; Search time 262.667 Seconds
(without alignments)
56.346 Million cell updates/sec

Title: US-10-763-712B-185
Perfect score: 45
Sequence: 1 XXXFXXXGGVMEAAXR 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries

Database : UniProt_7.2:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|------------|-------|---------------|--------|----|--------------|--------------------|
| 1 | 45 | 100.0 | 589 | 2 | Q9GTP2_TRIVA | Q9gtp2 trichomonas |
| 2 | 44 | 97.8 | 417 | 2 | Q3MXY8_9DELT | Q3mxy8 syntrophoba |
| 3 | 43 | 95.6 | 182 | 2 | Q68YU4_9CLOT | Q68yu4 uncultured |
| 4 | 43 | 95.6 | 182 | 2 | Q68YV0_9CLOT | Q68yv0 uncultured |

| | | | | | | |
|----|----|------|-----|---|--------------|--------------------|
| 5 | 43 | 95.6 | 182 | 2 | Q68YV1_9CLOT | Q68yv1 uncultured |
| 6 | 43 | 95.6 | 183 | 2 | Q68YU6_9CLOT | Q68yu6 uncultured |
| 7 | 43 | 95.6 | 183 | 2 | Q68YU7_9CLOT | Q68yu7 uncultured |
| 8 | 43 | 95.6 | 218 | 2 | Q2PWI4_9BACT | Q2pwi4 uncultured |
| 9 | 43 | 95.6 | 218 | 2 | Q2PWI5_9BACT | Q2pwi5 uncultured |
| 10 | 43 | 95.6 | 218 | 2 | Q2PWI9_9BACT | Q2pwi9 uncultured |
| 11 | 43 | 95.6 | 219 | 2 | Q2PWI6_9BACT | Q2pwi6 uncultured |
| 12 | 43 | 95.6 | 219 | 2 | Q38IH9_9BACT | Q38ih9 uncultured |
| 13 | 43 | 95.6 | 221 | 2 | Q2PWI1_9BACT | Q2pwi1 uncultured |
| 14 | 43 | 95.6 | 221 | 2 | Q2PWI3_9BACT | Q2pwi3 uncultured |
| 15 | 43 | 95.6 | 221 | 2 | Q38IH5_9BACT | Q38ih5 uncultured |
| 16 | 43 | 95.6 | 221 | 2 | Q38IH6_9BACT | Q38ih6 uncultured |
| 17 | 43 | 95.6 | 221 | 2 | Q38II2_9BACT | Q38ii2 uncultured |
| 18 | 43 | 95.6 | 221 | 2 | Q38II3_9BACT | Q38ii3 uncultured |
| 19 | 43 | 95.6 | 221 | 2 | Q38II5_9BACT | Q38ii5 uncultured |
| 20 | 43 | 95.6 | 221 | 2 | Q38II6_9BACT | Q38ii6 uncultured |
| 21 | 43 | 95.6 | 221 | 2 | Q38II8_9BACT | Q38ii8 uncultured |
| 22 | 43 | 95.6 | 221 | 2 | Q38IJ1_9BACT | Q38ij1 uncultured |
| 23 | 43 | 95.6 | 221 | 2 | Q38IJ3_9BACT | Q38ij3 uncultured |
| 24 | 43 | 95.6 | 222 | 2 | Q38II1_9BACT | Q38ii1 uncultured |
| 25 | 43 | 95.6 | 232 | 2 | Q5Y8D2_9CLOT | Q5y8d2 clostridium |
| 26 | 43 | 95.6 | 232 | 2 | Q5Y8D3_9CLOT | Q5y8d3 clostridium |
| 27 | 43 | 95.6 | 347 | 2 | Q3S2I8_9CLOT | Q3s2i8 ethanoligen |
| 28 | 43 | 95.6 | 387 | 2 | Q3GDU8_9FIRM | Q3gdu8 syntrophomo |
| 29 | 43 | 95.6 | 403 | 2 | Q9AU60_SCEOB | Q9au60 scenedesmus |
| 30 | 43 | 95.6 | 410 | 2 | Q2Z381_9GAMM | Q2z381 shewanella |
| 31 | 43 | 95.6 | 410 | 2 | Q364V4_9GAMM | Q364v4 shewanella |
| 32 | 43 | 95.6 | 410 | 2 | Q8EAI2_SHEON | Q8eai2 shewanella |
| 33 | 43 | 95.6 | 436 | 2 | Q8VX03_CHLFU | Q8vx03 chlorella f |
| 34 | 43 | 95.6 | 449 | 2 | Q9AR66_SCEOB | Q9ar66 scenedesmus |
| 35 | 43 | 95.6 | 456 | 2 | Q67J76_SYMTH | Q67j76 symbiobacte |
| 36 | 43 | 95.6 | 458 | 2 | Q56UD8_CHLMO | Q56ud8 chlamydomon |
| 37 | 43 | 95.6 | 471 | 2 | Q6AR16_DESPS | Q6ar16 desulfotale |
| 38 | 43 | 95.6 | 497 | 2 | Q9FYU1_CHLRE | Q9fyu1 chlamydomon |
| 39 | 43 | 95.6 | 505 | 2 | Q6T532_CHLRE | Q6t532 chlamydomon |
| 40 | 43 | 95.6 | 505 | 2 | Q6T533_CHLRE | Q6t533 chlamydomon |
| 41 | 43 | 95.6 | 505 | 2 | Q8VZZ0_CHLRE | Q8vzz0 chlamydomon |
| 42 | 43 | 95.6 | 527 | 2 | Q426A0_DESHA | Q426a0 desulfitoba |
| 43 | 43 | 95.6 | 563 | 2 | Q3GAL4_9FIRM | Q3gal4 syntrophomo |
| 44 | 43 | 95.6 | 572 | 2 | Q9ZNE4_CLOPE | Q9zne4 clostridium |
| 45 | 43 | 95.6 | 572 | 2 | Q9RHU8_CLOPE | Q9rhu8 clostridium |
| 46 | 43 | 95.6 | 573 | 2 | Q2RHS0_MOOTH | Q2rhs0 moorella th |
| 47 | 43 | 95.6 | 573 | 2 | Q3ZA52_DEHE1 | Q3za52 dehalococco |
| 48 | 43 | 95.6 | 573 | 2 | Q3ZWM9_DEHSC | Q3zwm9 dehalococco |
| 49 | 43 | 95.6 | 574 | 1 | PHF1_CLOPA | P29166 clostridium |
| 50 | 43 | 95.6 | 574 | 2 | Q3GAT5_9FIRM | Q3gat5 syntrophomo |
| 51 | 43 | 95.6 | 574 | 2 | Q3MXZ2_9DELT | Q3mxz2 syntrophoba |
| 52 | 43 | 95.6 | 574 | 2 | Q59261_CLOSA | Q59261 clostridium |
| 53 | 43 | 95.6 | 578 | 2 | Q93SF7_EUBAC | Q93sf7 eubacterium |
| 54 | 43 | 95.6 | 579 | 2 | Q2ZJ38_CALSA | Q2zj38 caldicellul |
| 55 | 43 | 95.6 | 579 | 2 | Q9XC55_CLOTM | Q9xc55 clostridium |
| 56 | 43 | 95.6 | 581 | 2 | Q3CJE2_THEET | Q3cje2 thermoanaer |
| 57 | 43 | 95.6 | 581 | 2 | Q8RBC8_THETN | Q8rbc8 thermoanaer |
| 58 | 43 | 95.6 | 582 | 2 | Q6F4C7_9CLOT | Q6f4c7 clostridium |
| 59 | 43 | 95.6 | 582 | 2 | Q4CDK8_CLOTM | Q4cdk8 clostridium |
| 60 | 43 | 95.6 | 582 | 2 | Q59262_CLOAB | Q59262 clostridium |
| 61 | 43 | 95.6 | 588 | 2 | Q8ABI6_BACTN | Q8abi6 bacteroides |
| 62 | 43 | 95.6 | 591 | 2 | Q3C5M2_9CLOT | Q3c5m2 alkaliphilu |
| 63 | 43 | 95.6 | 596 | 2 | Q67JF9_SYMTH | Q67jf9 symbiobacte |
| 64 | 43 | 95.6 | 596 | 2 | Q73MB6_TREDE | Q73mb6 treponema d |
| 65 | 43 | 95.6 | 598 | 2 | Q3A1L6_PELCD | Q3a1l6 pelobacter |

| | | | | | | |
|-----|----|------|------|---|--------------|--------------------|
| 66 | 43 | 95.6 | 605 | 2 | Q2LSB7_9DELT | Q2lsb7 syntrophus |
| 67 | 43 | 95.6 | 606 | 2 | Q46606_DESVU | Q46606 desulfovibr |
| 68 | 43 | 95.6 | 606 | 2 | Q72B67_DESVH | Q72b67 desulfovibr |
| 69 | 43 | 95.6 | 619 | 2 | Q370P7_RHOPA | Q370p7 rhodopseudo |
| 70 | 43 | 95.6 | 619 | 2 | Q6NDH4_RHOPA | Q6ndh4 rhodopseudo |
| 71 | 42 | 93.3 | 182 | 2 | Q68YU8_9CLOT | Q68yu8 uncultured |
| 72 | 42 | 93.3 | 220 | 2 | Q2PWI7_9BACT | Q2pwi7 uncultured |
| 73 | 42 | 93.3 | 220 | 2 | Q2PWJ8_9BACT | Q2pwj8 uncultured |
| 74 | 42 | 93.3 | 220 | 2 | Q38II4_9BACT | Q38ii4 uncultured |
| 75 | 42 | 93.3 | 230 | 2 | Q38IH8_9BACT | Q38ih8 uncultured |
| 76 | 42 | 93.3 | 389 | 2 | Q86ZE7_NEOFR | Q86ze7 neocallimas |
| 77 | 42 | 93.3 | 421 | 1 | PHFL_DESVH | P07598 desulfovibr |
| 78 | 42 | 93.3 | 421 | 1 | PHFL_DESVO | P13629 desulfovibr |
| 79 | 42 | 93.3 | 421 | 2 | O08311_DESFR | O08311 desulfovibr |
| 80 | 42 | 93.3 | 421 | 2 | Q9AM36_DESDE | Q9am36 desulfovibr |
| 81 | 42 | 93.3 | 421 | 2 | Q317L4_DESDG | Q317l4 desulfovibr |
| 82 | 42 | 93.3 | 439 | 2 | Q30Z18_DESDG | Q30z18 desulfovibr |
| 83 | 42 | 93.3 | 449 | 2 | Q27096_TRIVA | Q27096 trichomonas |
| 84 | 42 | 93.3 | 458 | 2 | Q315X0_DESDG | Q315x0 desulfovibr |
| 85 | 42 | 93.3 | 461 | 2 | Q2WUD6_CLOBE | Q2wud6 clostridium |
| 86 | 42 | 93.3 | 468 | 2 | Q27094_TRIVA | Q27094 trichomonas |
| 87 | 42 | 93.3 | 484 | 2 | Q9RGN3_MEGEL | Q9rgn3 megasphaera |
| 88 | 42 | 93.3 | 555 | 2 | Q8TG63_9FUNG | Q8tg63 piromyces s |
| 89 | 42 | 93.3 | 585 | 2 | Q3A430_PELCD | Q3a430 pelobacter |
| 90 | 42 | 93.3 | 608 | 2 | Q9WY44_THEMA | Q9wy44 thermotoga |
| 91 | 42 | 93.3 | 636 | 2 | Q8TFP2_NEOFR | Q8tfp2 neocallimas |
| 92 | 42 | 93.3 | 1198 | 2 | Q5DM85_NYCOV | Q5dm85 nyctotherus |
| 93 | 42 | 93.3 | 1206 | 2 | O96948_NYCOV | O96948 nyctotherus |
| 94 | 40 | 88.9 | 221 | 2 | Q2PWI0_9BACT | Q2pwi0 uncultured |
| 95 | 39 | 86.7 | 151 | 2 | Q62AB0_BURMA | Q62ab0 burkholderi |
| 96 | 39 | 86.7 | 156 | 2 | Q5Y8C9_9CLOT | Q5y8c9 clostridium |
| 97 | 39 | 86.7 | 156 | 2 | Q68YU5_9CLOT | Q68yu5 uncultured |
| 98 | 39 | 86.7 | 156 | 2 | Q68YV3_9CLOT | Q68yv3 uncultured |
| 99 | 39 | 86.7 | 156 | 2 | Q68YV4_9CLOT | Q68yv4 uncultured |
| 100 | 39 | 86.7 | 156 | 2 | Q68YV5_9CLOT | Q68yv5 uncultured |
| 101 | 39 | 86.7 | 170 | 2 | Q63NP9_BURPS | Q63np9 burkholderi |
| 102 | 39 | 86.7 | 171 | 2 | Q3X5V2_9ACTN | Q3x5v2 rubrobacter |
| 103 | 39 | 86.7 | 182 | 2 | Q68YV2_9CLOT | Q68yv2 uncultured |
| 104 | 39 | 86.7 | 186 | 2 | Q4AWQ7_9BURK | Q4awq7 polaromonas |
| 105 | 39 | 86.7 | 238 | 2 | Q5Y8D0_9CLOT | Q5y8d0 clostridium |
| 106 | 39 | 86.7 | 238 | 2 | Q5Y8D1_9CLOT | Q5y8d1 clostridium |
| 107 | 39 | 86.7 | 582 | 2 | Q3C9E8_9CLOT | Q3c9e8 alkaliphilu |
| 108 | 39 | 86.7 | 644 | 2 | Q2WI78_CLOBE | Q2wi78 clostridium |
| 109 | 38 | 84.4 | 585 | 2 | Q3A458_PELCD | Q3a458 pelobacter |
| 110 | 38 | 84.4 | 585 | 2 | Q46508_DESFR | Q46508 desulfovibr |
| 111 | 37 | 82.2 | 157 | 2 | Q8TVJ9_METKA | Q8tvj9 methanopyru |
| 112 | 37 | 82.2 | 159 | 2 | Q3Z8W3_DEHE1 | Q3z8w3 dehalococco |
| 113 | 37 | 82.2 | 159 | 2 | Q3ZX10_DEHSC | Q3zx10 dehalococco |
| 114 | 37 | 82.2 | 644 | 2 | Q4CDI0_CLOTM | Q4cdi0 clostridium |
| 115 | 37 | 82.2 | 1150 | 2 | Q420N6_DESHA | Q420n6 desulfitoba |
| 116 | 36 | 80.0 | 154 | 2 | Q3A2Y3_PELCD | Q3a2y3 pelobacter |
| 117 | 36 | 80.0 | 169 | 2 | Q8TMY5_METAC | Q8tmy5 methanosarc |
| 118 | 35 | 77.8 | 104 | 2 | Q2L9Z3_9CLOT | Q2l9z3 uncultured |
| 119 | 35 | 77.8 | 104 | 2 | Q2L9Z4_9CLOT | Q2l9z4 uncultured |
| 120 | 35 | 77.8 | 104 | 2 | Q2L9Z5_9CLOT | Q2l9z5 uncultured |
| 121 | 35 | 77.8 | 104 | 2 | Q2L9Z7_9CLOT | Q2l9z7 uncultured |
| 122 | 35 | 77.8 | 104 | 2 | Q2L9Z8_9CLOT | Q2l9z8 uncultured |
| 123 | 35 | 77.8 | 104 | 2 | Q2L9Z9_9CLOT | Q2l9z9 uncultured |
| 124 | 35 | 77.8 | 104 | 2 | Q2LA00_9CLOT | Q2la00 uncultured |
| 125 | 35 | 77.8 | 175 | 2 | Q40LF6_DESAC | Q40lf6 desulfuromo |
| 126 | 35 | 77.8 | 380 | 1 | T701_FREDI | Q00461 fremyella d |

| | | | | | | |
|-----|----|------|-----|---|--------------|--------------------|
| 127 | 35 | 77.8 | 566 | 2 | O83356_TREPA | O83356 treponema p |
| 128 | 34 | 75.6 | 104 | 2 | Q2L9Z6_9CLOT | Q2L9Z6 uncultured |
| 129 | 34 | 75.6 | 152 | 2 | Q33L36_METHU | Q33L36 methanospir |
| 130 | 34 | 75.6 | 156 | 2 | Q8PSK4_METMA | Q8psk4 methanosarc |
| 131 | 34 | 75.6 | 176 | 2 | Q469W1_METBA | Q469w1 methanosarc |
| 132 | 34 | 75.6 | 375 | 2 | Q8UKQ6_AGRT5 | Q8ukq6 agrobacteri |
| 133 | 34 | 75.6 | 388 | 2 | Q7D419_AGRT5 | Q7d419 agrobacteri |
| 134 | 34 | 75.6 | 390 | 2 | Q3ATR4_CHLCH | Q3atr4 chlorobium |
| 135 | 34 | 75.6 | 440 | 2 | Q5LTL3_SILPO | Q5ltl3 silicibacte |
| 136 | 34 | 75.6 | 706 | 2 | Q498X7_BRARE | Q498x7 brachydanio |
| 137 | 34 | 75.6 | 706 | 2 | Q8AW58_BRARE | Q8aw58 brachydanio |
| 138 | 34 | 75.6 | 766 | 2 | Q4DKD9_TRYCR | Q4dkd9 trypanosoma |
| 139 | 34 | 75.6 | 766 | 2 | Q4CVY5_TRYCR | Q4cvy5 trypanosoma |
| 140 | 34 | 75.6 | 820 | 2 | O45155_CAEEL | O45155 caenorhabdi |
| 141 | 33 | 73.3 | 117 | 2 | Q7XEE9_ORYSA | Q7xee9 oryza sativ |
| 142 | 33 | 73.3 | 151 | 2 | O29139_ARCFU | O29139 archaeoglob |
| 143 | 33 | 73.3 | 153 | 2 | Q3IU16_NATPD | Q3iu16 natronomona |
| 144 | 33 | 73.3 | 165 | 2 | Q3VXV2_9ACTO | Q3vxv2 fränkia sp. |
| 145 | 33 | 73.3 | 170 | 2 | Q3JHK8_BURP1 | Q3jhk8 burkholderi |
| 146 | 33 | 73.3 | 182 | 2 | Q4BTU9_BURVI | Q4btu9 burkholderi |
| 147 | 33 | 73.3 | 184 | 2 | Q44WD0_9BURK | Q44wd0 burkholderi |
| 148 | 33 | 73.3 | 184 | 2 | Q4LQR6_9BURK | Q4lqr6 burkholderi |
| 149 | 33 | 73.3 | 356 | 2 | Q2JPT3_9CYAN | Q2jpt3 cyanobacter |
| 150 | 33 | 73.3 | 356 | 2 | Q2JW91_9CYAN | Q2jw91 cyanobacter |

ALIGNMENTS

RESULT 1

Q9GTP2_TRIVA

ID Q9GTP2_TRIVA PRELIMINARY; PRT; 589 AA.

AC Q9GTP2;

DT 01-MAR-2001, integrated into UniProtKB/TrEMBL.

DT 01-MAR-2001, sequence version 1.

DT 07-FEB-2006, entry version 23.

DE Putative 64kDa iron hydrogenase (Fragment).

OS Trichomonas vaginalis.

OC Eukaryota; Parabasalidea; Trichomonada; Trichomonadida;

OC Trichomonadidae; Trichomonadinae; Trichomonas.

OX NCBI_TaxID=5722;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RX MEDLINE=20523972; PubMed=11070057;

RA Horner D.S., Foster P.G., Embley M.T.;

RT "Iron hydrogenases and the evolution of anaerobic eukaryotes.";

RL Mol. Biol. Evol. 17:1695-1709(2000).

CC -!- SUBCELLULAR LOCATION: Periplasmic (By similarity).

CC

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CC

DR EMBL; AF262401; AAG31037.1; -; mRNA.

DR HSSP; P07598; 1HFE.

DR GO; GO:0042597; C:periplasmic space; IEA.

DR GO; GO:0051539; F:4 iron, 4 sulfur cluster binding; IEA.

DR GO; GO:0005489; F:electron transporter activity; IEA.

DR GO; GO:0008901; F:ferredoxin hydrogenase activity; IEA.

DR GO; GO:0005506; F:iron ion binding; IEA.

DR GO; GO:0046872; F:metal ion binding; IEA.

DR GO; GO:0016491; F:oxidoreductase activity; IEA.

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This page gives you Search Results detail for the Application 10763712 and Search Result us-10-712
[start](#)

A;Cross-references: UNIPROT:O83356; UNIPARC:UPI00000D3239; GB:AE001213; GB:AE000520;
- Agrobacterium tumefaciens (strain C58, Dupont) plasmid AT C;Species: Agrobacterium tumefaciens
A.; Raymond, C.; Rouse, G.; Saenphimmachak, C.; Wu, Z.; Gordon, D.; Eisen, J.A.; Paulsen, I.; K
PMID:11743193 A;Accession: AB3165 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-
FXXXGGVMEAAXR 16 || :||| | Db 173 FDTSGGYVEAAVR 185 RESULT 13 G88996 protein C17B7.5
PMID:9851916 A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/Pr
C17B7.5 A;Map position: 5 Query Match 75.6%; Score 34; DB 2; Length 820; Best Local Similarity
O.; Nelson, K.E.; Ketchum, K.A.; Dodson, R.J.; Gwinn, M.; Hickey, E.K.; Peterson, J.D.; Richards
Artiach, P.; Kaine, B.P.; Sykes, S.M.; Sadow, P.W.; D'Andrea, K.P.; Bowman, C.; Fujii, C.; Garland
A;Cross-references: UNIPROT:O29139; UNIPARC:UPI0000056E45; GB:AE001026; GB:AE000782;
pombe C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004 C;Acces
SPDB:SPCC285.11 A;Experimental source: strain 972h-; cosmid c285 C;Genetics: A;Gene: SPDB:5
#text_change 18-Feb-2000 C;Accession: D36144 R;Crouzet, J.; Cauchois, L.; Blanche, F.; Debuss
MUID:91008975; PMID:2211520 A;Accession: D36144 A;Status: preliminary A;Molecule type: DN
RESULT 17 JC4118 probable site-specific integrase - phage Cf1t N;Alternate names: ORF344 C;Spe
A;Accession: JC4118 A;Molecule type: DNA A;Residues: 1-344 A;Cross-references: UNIPROT:Q379
disease in orange. C;Genetics: A;Start codon: GTG C;Superfamily: phage Cf1t integrase C;Keywo
Xanthomonas campestris C;Date: 08-Mar-1996 #sequence_revision 19-Apr-1996 #text_change 20
UNIPARC:UPI000009B339; GB:U38235; NID:g1185453; PIDN:AAC54630.1; PID:g1185454 A;Expe
53.8%; Pred. No. 34; Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0; Qy 4 FXXXGGV
F.S.L.; Hufnagle, W.O.; Kowalik, D.J.; Lagrou, M.; Garber, R.L.; Goltry, L.; Tolentino, E.; Westbro
PMID:10984043 A;Accession: E83637 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-2
66.7%; Pred. No. 40; Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0; Qy 8 GGVMEAA
R.A.; Short, J.M.; Olson, G.J.; Swanson, R.V. Nature 392, 353-358, 1998 A;Title: The complete ge
GB:AE000657 A;Experimental source: strain VF5 C;Genetics: A;Gene: aq_1884 Query Match 68.9
C72672 R;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takaha
Aeropyrum pernix K1. A;Reference number: A72450; MUID:99310339; PMID:10382966 A;Accessio
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0; Qy 8 GGVMEAAXR 16 || :||| | Db 138
Couve, E.; de Daruvar, A.; Dehoux, P.; Domann, E.; Dominguez-Bernal, G.; Duchaud, E.; Durand,
Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, J.; Cossart, P. A;1
C;Superfamily: short protease IV-related protein Query Match 68.9%; Score 31; DB 2; Length 337
L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, H.; Brandt, P.; Chakraborty, T.; C
A.; Mata Vicente, J.; Ng, E.; Nordsiek, G.; Novella, S.; de Pablos, B.; Perez-Diaz, J.C.; R Emmel, B.
PIDN:CAC96858.1; PID:g16414114; GSPDB:GN00178 A;Experimental source: strain Clip11262 C;
(strain PAO1) C;Species: Pseudomonas aeruginosa C;Date: 15-Sep-2000 #sequence_revision 15-9
I.T.; Reizer, J.; Saier, M.H.; Hancock, R.E.W.; Lory, S.; Olson, M.V. Nature 406, 959-964, 2000 A;
PASP:PA1410 A;Experimental source: strain PAO1 C;Genetics: A;Gene: PA1410 C;Superfamily: sp
#sequence_revision 20-Apr-2001 #text_change 09-Jul-2004 C;Accession: F87508 R;Nierman, W.C
Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141,
conserved probable membrane protein YIL003w Query Match 68.9%; Score 31; DB 2; Length 366;
C;Accession: A98315 R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quorllo, B.
Agrobacterium tumefaciens C58. A;Reference number: A97359; MUID:21608551; PMID:11743194
Conservative 2; Mismatches 1; Indels 0; Gaps 0; Qy 8 GGVMEAAXR 16 |||:| | Db 273 GGVVEASC
Zhou, Y.; Bovee Sr., D.; Chapman, P.; Clendenning, J.; Deatherage, G.; Gillet, W.; Grant, C.; Guer
Olson, M.V.; Nester, E.W. A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tum
chromosome Query Match 68.9%; Score 31; DB 2; Length 377; Best Local Similarity 66.7%; Pred.

carboxyvinyltransferase (EC 2.5.1.19); shikimate 5-dehydrogenase (EC 1.1.1.25); shikimate kinase
MUID:88076802; PMID:2825635 A;Accession: A32519 A;Molecule type: DNA A;Residues: 1-1588
GSPDB:GN00004; MIPS:YDR127w R;Duncan, K.; Edwards, R.M.; Coggins, J.R. FEBS Lett. 241, 83-
A;Gene: SGD:ARO1; MIPS:YDR127w A;Cross-references: SGD:S0002534; MIPS:YDR127w A;Map |
phosphorus-oxygen lyase; phosphotransferase F;7-380/Domain: 3-dehydroquinase synthase homo
Gaps 0; Qy 4 FXXXGGVMEAA 14 ||::|| Db 966 FSTGGGIVESA 976 RESULT 29 D97316 probable
Bennett, G.N.; Koonin, E.V.; Smith, D.R. J. Bacteriol. 183, 4823-4838, 2001 A;Title: Genome Sequ
Clostridium acetobutylicum ATCC824 C;Genetics: A;Gene: CAC3389 Query Match 68.9%; Score 31
14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 05-Oct-2004 C;Accession: AH2414 F
Anabaena sp. strain PCC 7120. A;Reference number: AB1807; MUID:21595285; PMID:11759840 A
40; Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0; Qy 8 GGVMEAAAXR 16 ||::|| Db

GenCore version 5.1.9

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OM protein - protein search, using sw model

Run on: June 29, 2006, 08:24:08 ; Search time 31.3333 Seconds
(without alignments)
49.132 Million cell updates/sec

Title: US-10-763-712B-185
Perfect score: 45
Sequence: 1 XXXFXXXGGVMEAAAXR 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries

Database : PIR_80:*
1: pirl:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query | | DB | ID | Description |
|---------------|-------|------------|--------|----|--------|--------------------|
| | | Match | Length | | | |
| 1 | 43 | 95.6 | 574 | 1 | HQCL1P | hydrogenase (EC 1. |
| 2 | 43 | 95.6 | 582 | 2 | D96903 | hydrogene dehydrog |
| 3 | 43 | 95.6 | 582 | 2 | JC6002 | hydrogenase (EC 1. |
| 4 | 43 | 95.6 | 606 | 2 | S13526 | hydrogenase (EC 1. |
| 5 | 42 | 93.3 | 421 | 1 | HQDVFL | cytochrome-c3 hydr |
| 6 | 42 | 93.3 | 421 | 1 | HQDVLV | cytochrome-c3 hydr |

| | | | | | | |
|----|----|------|------|---|--------|------------------------|
| 7 | 42 | 93.3 | 608 | 2 | C72405 | hydrogenase (EC 1. |
| 8 | 42 | 93.3 | 1206 | 2 | T18557 | probable hydrogenase |
| 9 | 38 | 84.4 | 585 | 2 | D57150 | hydrogenase (EC 1. |
| 10 | 35 | 77.8 | 380 | 2 | S16891 | probable transposase |
| 11 | 35 | 77.8 | 566 | 2 | F71337 | probable comE protein |
| 12 | 34 | 75.6 | 375 | 2 | AB3165 | conserved hypothetical |
| 13 | 34 | 75.6 | 820 | 2 | G88996 | protein C17B7.5 [i |
| 14 | 33 | 73.3 | 151 | 2 | E69390 | P450 cytochrome h |
| 15 | 33 | 73.3 | 427 | 2 | T41257 | hypothetical prote |
| 16 | 32 | 71.1 | 333 | 2 | D36144 | cobC protein - Pse |
| 17 | 32 | 71.1 | 344 | 1 | JC4118 | probable site-spec |
| 18 | 32 | 71.1 | 346 | 2 | JC4582 | replication initia |
| 19 | 31 | 68.9 | 242 | 2 | E83637 | probable phosphopr |
| 20 | 31 | 68.9 | 250 | 2 | D70462 | conserved hypothet |
| 21 | 31 | 68.9 | 293 | 2 | C72672 | probable survival |
| 22 | 31 | 68.9 | 337 | 2 | AI1272 | proteinase homolog |
| 23 | 31 | 68.9 | 337 | 2 | AB1636 | proteinases homolo |
| 24 | 31 | 68.9 | 363 | 2 | A83470 | probable periplasm |
| 25 | 31 | 68.9 | 366 | 2 | F87508 | GTP-binding protei |
| 26 | 31 | 68.9 | 377 | 2 | A98315 | hypothetical prote |
| 27 | 31 | 68.9 | 377 | 2 | AB2968 | conserved hypothet |
| 28 | 31 | 68.9 | 1588 | 1 | BVBYA1 | 3-dehydroquinat |
| 29 | 31 | 68.9 | 1939 | 2 | D97316 | probable S-layer p |
| 30 | 30 | 66.7 | 147 | 2 | AH2414 | hypothetical prote |
| 31 | 30 | 66.7 | 230 | 2 | E95017 | ABC transporter, p |
| 32 | 30 | 66.7 | 230 | 2 | F97890 | hypothetical prote |
| 33 | 30 | 66.7 | 244 | 2 | T39507 | probable ATP synth |
| 34 | 30 | 66.7 | 261 | 2 | D98256 | hypothetical prote |
| 35 | 30 | 66.7 | 261 | 2 | AG3028 | hypothetical prote |
| 36 | 30 | 66.7 | 274 | 2 | F86264 | proteasome endopep |
| 37 | 30 | 66.7 | 306 | 2 | F69129 | tungsten formylmet |
| 38 | 30 | 66.7 | 323 | 2 | E86935 | conserved hypothet |
| 39 | 30 | 66.7 | 356 | 2 | H82639 | hypothetical prote |
| 40 | 30 | 66.7 | 362 | 2 | A49316 | chorismate synthas |
| 41 | 30 | 66.7 | 377 | 2 | F69008 | acetyltransferase |
| 42 | 30 | 66.7 | 475 | 2 | H84137 | hypothetical prote |
| 43 | 30 | 66.7 | 631 | 2 | H70835 | hypothetical prote |
| 44 | 30 | 66.7 | 650 | 2 | AE1992 | ABC transporter AT |
| 45 | 30 | 66.7 | 695 | 2 | G64327 | H+-transporting tw |
| 46 | 30 | 66.7 | 839 | 2 | F85334 | myosin heavy chain |
| 47 | 30 | 66.7 | 1101 | 2 | G83637 | hypothetical prote |
| 48 | 30 | 66.7 | 1175 | 2 | T20346 | pyruvate carboxyla |
| 49 | 30 | 66.7 | 1178 | 1 | A47255 | pyruvate carboxyla |
| 50 | 30 | 66.7 | 1178 | 1 | JC2460 | pyruvate carboxyla |
| 51 | 30 | 66.7 | 1178 | 2 | JC4391 | pyruvate carboxyla |
| 52 | 30 | 66.7 | 1195 | 2 | T43735 | pyruvate carboxyla |
| 53 | 30 | 66.7 | 1446 | 2 | T04528 | myosin heavy chain |
| 54 | 30 | 66.7 | 1477 | 2 | T00957 | myosin heavy chain |
| 55 | 30 | 66.7 | 1515 | 2 | S51824 | myosin heavy chain |
| 56 | 30 | 66.7 | 1611 | 2 | A84743 | probable myosin he |
| 57 | 30 | 66.7 | 1643 | 2 | T07961 | myosin heavy chain |
| 58 | 30 | 66.7 | 1736 | 2 | F86178 | hypothetical prote |
| 59 | 30 | 66.7 | 1738 | 2 | C84507 | hypothetical prote |
| 60 | 29 | 64.4 | 175 | 2 | H71249 | hypothetical prote |
| 61 | 29 | 64.4 | 181 | 2 | AE0018 | probable hydrolase |
| 62 | 29 | 64.4 | 188 | 2 | E75365 | kanamycin resistan |
| 63 | 29 | 64.4 | 228 | 2 | D84261 | hypothetical prote |
| 64 | 29 | 64.4 | 260 | 2 | G87349 | conserved hypothet |
| 65 | 29 | 64.4 | 320 | 2 | JC7929 | ATP-dependent gluc |
| 66 | 29 | 64.4 | 376 | 2 | F72514 | probable glucokina |
| 67 | 29 | 64.4 | 379 | 2 | AI1391 | UDP-N-acetylglucos |

| | | | | | | |
|-----|----|------|------|---|--------|---------------------|
| 68 | 29 | 64.4 | 379 | 2 | AC1767 | UDP-N-acetylglucos |
| 69 | 29 | 64.4 | 387 | 2 | F82692 | conserved hypothet |
| 70 | 29 | 64.4 | 406 | 2 | A69553 | conserved hypothet |
| 71 | 29 | 64.4 | 413 | 2 | A95874 | probable D-amino-a |
| 72 | 29 | 64.4 | 433 | 1 | S22284 | transcription regu |
| 73 | 29 | 64.4 | 500 | 2 | T22068 | hypothetical prote |
| 74 | 29 | 64.4 | 507 | 2 | AF0974 | phosphoglycerate m |
| 75 | 29 | 64.4 | 514 | 2 | C86037 | hypothetical prote |
| 76 | 29 | 64.4 | 514 | 2 | B91190 | hypothetical prote |
| 77 | 29 | 64.4 | 514 | 2 | S47833 | probable phosphogl |
| 78 | 29 | 64.4 | 633 | 2 | AD1116 | internalin, probab |
| 79 | 29 | 64.4 | 748 | 2 | T47250 | complex I intermed |
| 80 | 29 | 64.4 | 750 | 2 | E84475 | probable Athila re |
| 81 | 29 | 64.4 | 783 | 2 | AG3402 | polyphosphate kina |
| 82 | 29 | 64.4 | 999 | 2 | AG2413 | hypothetical prote |
| 83 | 29 | 64.4 | 1176 | 2 | S66771 | hypothetical prote |
| 84 | 29 | 64.4 | 1677 | 2 | T46095 | hypothetical prote |
| 85 | 29 | 64.4 | 2201 | 2 | AH0095 | probable sideropho |
| 86 | 28 | 62.2 | 70 | 2 | S25190 | pilin precursor - |
| 87 | 28 | 62.2 | 100 | 2 | S72816 | hypothetical prote |
| 88 | 28 | 62.2 | 113 | 2 | T30041 | hypothetical prote |
| 89 | 28 | 62.2 | 128 | 2 | T28433 | selenophosphate sy |
| 90 | 28 | 62.2 | 152 | 2 | S57421 | cysteine proteinas |
| 91 | 28 | 62.2 | 155 | 2 | AD2801 | bacterioferritin c |
| 92 | 28 | 62.2 | 155 | 2 | F97580 | bacterioferritin c |
| 93 | 28 | 62.2 | 166 | 2 | I53166 | leptin precursor - |
| 94 | 28 | 62.2 | 167 | 1 | LTHU | leptin precursor - |
| 95 | 28 | 62.2 | 172 | 2 | JE0392 | inorganic diphosph |
| 96 | 28 | 62.2 | 173 | 2 | A70017 | 4-hydroxybenzoyl-C |
| 97 | 28 | 62.2 | 181 | 2 | S39717 | ywdL protein - Bac |
| 98 | 28 | 62.2 | 185 | 2 | A64159 | intracellular sept |
| 99 | 28 | 62.2 | 201 | 2 | B81421 | hypothetical prote |
| 100 | 28 | 62.2 | 210 | 2 | C81216 | conserved hypothet |
| 101 | 28 | 62.2 | 210 | 2 | G81793 | hypothetical prote |
| 102 | 28 | 62.2 | 223 | 2 | E75390 | phage shock protei |
| 103 | 28 | 62.2 | 264 | 2 | E81127 | hypothetical prote |
| 104 | 28 | 62.2 | 264 | 2 | H81834 | hypothetical prote |
| 105 | 28 | 62.2 | 268 | 2 | AD2622 | conserved hypothet |
| 106 | 28 | 62.2 | 276 | 2 | AE3543 | 3-isopropylmalate |
| 107 | 28 | 62.2 | 285 | 2 | A84224 | cytochrome c oxida |
| 108 | 28 | 62.2 | 293 | 2 | E83749 | glucose kinase BH0 |
| 109 | 28 | 62.2 | 296 | 2 | A95276 | probable KduI DKI |
| 110 | 28 | 62.2 | 306 | 2 | D97404 | probable dapE gene |
| 111 | 28 | 62.2 | 323 | 2 | B70561 | probable mesJ prot |
| 112 | 28 | 62.2 | 325 | 2 | I57009 | 3-Hydroxy-3-methyl |
| 113 | 28 | 62.2 | 331 | 2 | F84049 | proteinase IV BH31 |
| 114 | 28 | 62.2 | 334 | 2 | C87508 | HlyD family secret |
| 115 | 28 | 62.2 | 336 | 2 | AD0781 | galactoside transp |
| 116 | 28 | 62.2 | 336 | 2 | B85853 | hypothetical prote |
| 117 | 28 | 62.2 | 336 | 2 | C37277 | transmembrane pore |
| 118 | 28 | 62.2 | 336 | 2 | H91008 | hypothetical prote |
| 119 | 28 | 62.2 | 336 | 2 | I64096 | transmembrane pore |
| 120 | 28 | 62.2 | 336 | 2 | AI0183 | galactoside permea |
| 121 | 28 | 62.2 | 337 | 2 | F82214 | galactoside ABC tr |
| 122 | 28 | 62.2 | 348 | 2 | T51781 | protein kinase AtPP |
| 123 | 28 | 62.2 | 349 | 2 | D70543 | probable nadA prot |
| 124 | 28 | 62.2 | 352 | 2 | C84199 | hypothetical prote |
| 125 | 28 | 62.2 | 356 | 2 | B39798 | RP2 protein, testo |
| 126 | 28 | 62.2 | 357 | 2 | A39798 | RP2 protein, testo |
| 127 | 28 | 62.2 | 357 | 2 | A23641 | RP2 protein, testo |
| 128 | 28 | 62.2 | 362 | 1 | S12581 | cysteine proteinas |

SCORE Search Results Details for Application 10763712 and Search Result us-10-763-712b 185.rnpbn.

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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 29, 2006, 20:17:32 ; Search time 111.333 Seconds
(without alignments)
254.909 Million cell updates/sec

Title: US-10-763-712B-185
Perfect score: 45
Sequence: 1 XXXFXXXGGVMEAAAXR 16

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 809770 seqs, 591248006 residues

Total number of hits satisfying chosen parameters: 1619540

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries

Command line parameters:

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-MODEL=frame+ p2n.model -DEV=xlh
-Q=/abss/ABSSWEB_spool/US10763712/runat_29062006_075109_19603/app_query.fasta_1
-DB=Published_Applications_NA_New -QFMT=fastap -SUFFIX=rnpbn -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=150 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=25 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -HOST=abss03h
-USER=US10763712 @CGN_1_1_154 @runat_29062006_075109_19603 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Database : Published_Applications_NA_New:*
1: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US09_NEW_PUB.seq:*

2: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US06_NEW_PUB.seq:*
 3: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US07_NEW_PUB.seq:*
 4: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US08_NEW_PUB.seq:*
 5: /EMC_Celerra_SIDS3/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
 6: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US10_NEW_PUB.seq:*
 7: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq:*
 8: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result | | | % | | Query | | DB | ID | Description |
|--------|-----|-------|-------|--------|--------|-----------------------|----|----|-------------------|
| | No. | Score | Match | Length | Length | Score | | | |
| c | 1 | 36 | 80.0 | 1630 | 6 | US-10-449-902-12209 | | | Sequence 12209, A |
| | 2 | 35 | 77.8 | 974 | 6 | US-10-449-902-15171 | | | Sequence 15171, A |
| c | 3 | 35 | 77.8 | 1435 | 6 | US-10-449-902-7815 | | | Sequence 7815, Ap |
| c | 4 | 35 | 77.8 | 1497 | 6 | US-10-449-902-21825 | | | Sequence 21825, A |
| c | 5 | 35 | 77.8 | 1516 | 6 | US-10-449-902-20898 | | | Sequence 20898, A |
| c | 6 | 34 | 75.6 | 1628 | 6 | US-10-449-902-14499 | | | Sequence 14499, A |
| c | 7 | 34 | 75.6 | 1628 | 6 | US-10-449-902-21751 | | | Sequence 21751, A |
| c | 8 | 33 | 73.3 | 907 | 7 | US-11-266-748A-480315 | | | Sequence 480315, |
| c | 9 | 33 | 73.3 | 914 | 6 | US-10-449-902-16607 | | | Sequence 16607, A |
| c | 10 | 33 | 73.3 | 926 | 7 | US-11-266-748A-86752 | | | Sequence 86752, A |
| | 11 | 33 | 73.3 | 926 | 7 | US-11-266-748A-139563 | | | Sequence 139563, |
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| | 13 | 33 | 73.3 | 1135 | 7 | US-11-266-748A-450288 | | | Sequence 450288, |
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| c | 20 | 31 | 68.9 | 309 | 7 | US-11-284-817-3 | | | Sequence 3, Appli |
| c | 21 | 31 | 68.9 | 337 | 7 | US-11-222-565-56 | | | Sequence 56, Appl |
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| c 115 | 31 | 68.9 | 13042 | 7 | US-11-236-836-17 | Sequence 17, Appl |
| c 116 | 31 | 68.9 | 13042 | 7 | US-11-236-836-23 | Sequence 23, Appl |
| c 117 | 31 | 68.9 | 13147 | 7 | US-11-236-836-18 | Sequence 18, Appl |
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| 125 | 30 | 66.7 | 585 | 7 | US-11-266-748A-442635 | Sequence 442635, |
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| 137 | 30 | 66.7 | 1000 | 7 | US-11-266-748A-292880 | Sequence 292880, |
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| 139 | 30 | 66.7 | 1000 | 7 | US-11-266-748A-404723 | Sequence 404723, |
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| c 147 | 30 | 66.7 | 1099 | 7 | US-11-266-748A-249547 | Sequence 249547, |
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| c 149 | 30 | 66.7 | 1312 | 6 | US-10-449-902-20490 | Sequence 20490, A |
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ALIGNMENTS

RESULT 1

US-10-449-902-12209/c

; Sequence 12209, Application US/10449902

; Publication No. US20060123505A1

; GENERAL INFORMATION:

; APPLICANT: National Institute of Agrobiological Sciences.

; APPLICANT: Bio-oriented Technology Research Advancement Institution.

; APPLICANT: The Institute of Physical and Chemical Research.

; APPLICANT: Foundation for Advancement of International Science.

; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF

; FILE REFERENCE: MOA-A0205Y1-US

; CURRENT APPLICATION NUMBER: US/10/449,902

Comments /
Suggestions

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SUMMARIES

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| 5 | 44 | 97.8 | 39 | 9 | US-10-411-910A-313 | Sequence 313, App |
| 6 | 44 | 97.8 | 39 | 9 | US-10-411-910A-319 | Sequence 319, App |
| 7 | 44 | 97.8 | 39 | 9 | US-10-411-910A-323 | Sequence 323, App |
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| 14 | 43 | 95.6 | 39 | 9 | US-10-411-910A-327 | Sequence 327, App |
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| 17 | 43 | 95.6 | 1212 | 9 | US-10-411-910A-222 | Sequence 222, App |
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| 29 | 43 | 95.6 | 1494 | 9 | US-10-411-910A-219 | Sequence 219, App |
| 30 | 43 | 95.6 | 1494 | 10 | US-10-763-712A-173 | Sequence 173, App |
| 31 | 43 | 95.6 | 1518 | 9 | US-10-411-910A-114 | Sequence 114, App |
| 32 | 43 | 95.6 | 1518 | 9 | US-10-411-910A-221 | Sequence 221, App |
| 33 | 43 | 95.6 | 1665 | 9 | US-10-411-910A-122 | Sequence 122, App |
| 34 | 43 | 95.6 | 1665 | 9 | US-10-411-910A-229 | Sequence 229, App |
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| 48 | 43 | 95.6 | 1740 | 8 | US-10-282-122A-16510 | Sequence 16510, A |
| 49 | 43 | 95.6 | 1746 | 9 | US-10-411-910A-116 | Sequence 116, App |
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| 67 | 42 | 93.3 | 39 | 9 | US-10-411-910A-285 | Sequence 285, App |
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| 79 | 42 | 93.3 | 1265 | 10 | US-10-763-712A-175 | Sequence 175, App |
| 80 | 42 | 93.3 | 1266 | 9 | US-10-411-910A-90 | Sequence 90, Appl |
| 81 | 42 | 93.3 | 1266 | 9 | US-10-411-910A-95 | Sequence 95, Appl |
| 82 | 42 | 93.3 | 1266 | 9 | US-10-411-910A-101 | Sequence 101, App |
| 83 | 42 | 93.3 | 1266 | 9 | US-10-411-910A-103 | Sequence 103, App |
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| 86 | 42 | 93.3 | 1266 | 9 | US-10-411-910A-202 | Sequence 202, App |
| 87 | 42 | 93.3 | 1266 | 9 | US-10-411-910A-208 | Sequence 208, App |
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| 102 | 42 | 93.3 | 1827 | 9 | US-10-411-910A-104 | Sequence 104, App |
| 103 | 42 | 93.3 | 1827 | 9 | US-10-411-910A-211 | Sequence 211, App |
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| 105 | 42 | 93.3 | 1911 | 9 | US-10-411-910A-225 | Sequence 225, App |
| 106 | 42 | 93.3 | 3621 | 9 | US-10-411-910A-106 | Sequence 106, App |
| 107 | 42 | 93.3 | 3621 | 9 | US-10-411-910A-213 | Sequence 213, App |
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| 117 | 37 | 82.2 | 1935 | 9 | US-10-411-910A-232 | Sequence 232, App |
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| c 128 | 35 | 77.8 | 3011 | 8 | US-10-437-963-40436 | Sequence 40436, A |
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| 131 | 35 | 77.8 | 4341 | 10 | US-10-499-353A-248 | Sequence 248, App |
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| 135 | 35 | 77.8 | 7728 | 10 | US-10-499-353A-245 | Sequence 245, App |
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| 143 | 34 | 75.6 | 370 | 3 | US-09-917-800A-455 | Sequence 455, App |
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| 146 | 34 | 75.6 | 561 | 4 | US-09-925-065A-200209 | Sequence 200209, |
| 147 | 34 | 75.6 | 561 | 5 | US-09-925-065A-200209 | Sequence 200209, |
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ALIGNMENTS

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US-10-411-910A-110
; Sequence 110, Application US/10411910A

SCORE Search Results Details for Application 10763712 and Search Result us-10-763-712b- 185.rni.

| | | | | |
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| Score Home | Retrieve Application | SCORE System | SCORE | Comments / |
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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 29, 2006, 20:00:56 ; Search time 146 Seconds
(without alignments)
307.580 Million cell updates/sec

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Sequence: 1 XXXFXXXGGVMEAAAXR 16

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Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 4 | 43 | 95.6 | 3265 | 3 | US-10-077-699C-3 | Sequence 3, Appli |
| 5 | 43 | 95.6 | 5001 | 3 | US-10-077-699C-1 | Sequence 1, Appli |
| 6 | 43 | 95.6 | 5208 | 3 | US-10-077-699C-2 | Sequence 2, Appli |
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| 13 | 33 | 73.3 | 936 | 3 | US-09-902-540-4133 | Sequence 4133, Ap |
| 14 | 33 | 73.3 | 1169 | 3 | US-09-902-540-332 | Sequence 332, App |
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| 16 | 33 | 73.3 | 18469 | 3 | US-09-902-540-1205 | Sequence 1205, Ap |
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| 18 | 32 | 71.1 | 441 | 3 | US-08-914-375C-50 | Sequence 50, Appl |
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| 21 | 32 | 71.1 | 601 | 3 | US-09-949-016-94397 | Sequence 94397, A |
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| c 132 | 31 | 68.9 | 244 | 3 | US-09-676-768-29 | Sequence 29, Appl |
| c 133 | 31 | 68.9 | 244 | 3 | US-09-676-768-31 | Sequence 31, Appl |
| c 134 | 31 | 68.9 | 252 | 3 | US-08-441-971-33 | Sequence 33, Appl |
| c 135 | 31 | 68.9 | 252 | 3 | US-08-441-971-34 | Sequence 34, Appl |
| c 136 | 31 | 68.9 | 252 | 3 | US-08-441-971-35 | Sequence 35, Appl |
| c 137 | 31 | 68.9 | 252 | 3 | US-08-441-971-36 | Sequence 36, Appl |
| c 138 | 31 | 68.9 | 252 | 3 | US-08-441-971-37 | Sequence 37, Appl |
| c 139 | 31 | 68.9 | 252 | 3 | US-08-441-971-38 | Sequence 38, Appl |
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| c 141 | 31 | 68.9 | 252 | 3 | US-08-441-971-40 | Sequence 40, Appl |
| c 142 | 31 | 68.9 | 252 | 3 | US-08-441-971-41 | Sequence 41, Appl |
| c 143 | 31 | 68.9 | 252 | 3 | US-08-441-971-42 | Sequence 42, Appl |
| c 144 | 31 | 68.9 | 252 | 3 | US-08-441-971-43 | Sequence 43, Appl |
| c 145 | 31 | 68.9 | 252 | 3 | US-08-441-971-44 | Sequence 44, Appl |
| c 146 | 31 | 68.9 | 252 | 3 | US-08-441-971-45 | Sequence 45, Appl |
| c 147 | 31 | 68.9 | 252 | 3 | US-08-441-971-48 | Sequence 48, Appl |
| c 148 | 31 | 68.9 | 252 | 3 | US-08-441-971-49 | Sequence 49, Appl |
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ALIGNMENTS

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 US-10-077-699C-8
 ; Sequence 8, Application US/10077699C
 ; Patent No. 6858718
 ; GENERAL INFORMATION:
 ; APPLICANT: Happe, Thomas
 ; TITLE OF INVENTION: Hydrogen Production
 ; FILE REFERENCE: 01MEL1
 ; CURRENT APPLICATION NUMBER: US/10/077,699C
 ; CURRENT FILING DATE: 2002-02-15

SCORE Search Results Details for Application 10763712 and Search Result us-10-763-712b-185.rng.

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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 29, 2006, 19:28:24 ; Search time 529.333 Seconds
(without alignments)
316.122 Million cell updates/sec

Title: US-10-763-712B-185
Perfect score: 45
Sequence: 1 XXXFXXXGGVMEAAXR 16

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries

Command line parameters:

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-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=150
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-USER=US10763712 @CGN_1_1_942 @runat_29062006_075054_19188 -NCPU=6 -ICPU=3
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 4 | 44 | 97.8 | 39 | 13 | ADT91279 | Adt91279 Fe-hydrog |
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| 6 | 43 | 95.6 | 39 | 13 | ADT91300 | Adt91300 Fe-hydrog |
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| 11 | 43 | 95.6 | 39 | 13 | ADT91294 | Adt91294 Fe-hydrog |
| 12 | 43 | 95.6 | 39 | 13 | ADT91298 | Adt91298 Fe-hydrog |
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| 14 | 43 | 95.6 | 39 | 13 | ADT91280 | Adt91280 Fe-hydrog |
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| 16 | 43 | 95.6 | 1350 | 14 | AEB73391 | Aeb73391 DNA encod |
| 17 | 43 | 95.6 | 1494 | 14 | AEB73387 | Aeb73387 cDNA enco |
| 18 | 43 | 95.6 | 1725 | 14 | AEB73388 | Aeb73388 cDNA enco |
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| 20 | 43 | 95.6 | 1737 | 2 | AAZ25199 | Aaz25199 Clostridi |
| 21 | 43 | 95.6 | 1740 | 8 | ACA28640 | Aca28640 Prokaryot |
| 22 | 43 | 95.6 | 1749 | 8 | ACA27971 | Aca27971 Prokaryot |
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| 24 | 43 | 95.6 | 2347 | 10 | ADC59543 | Adc59543 Clostridi |
| 25 | 43 | 95.6 | 2347 | 13 | ADR90306 | Adr90306 Clostridi |
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| 36 | 42 | 93.3 | 39 | 13 | ADT91287 | Adt91287 Fe-hydrog |
| 37 | 42 | 93.3 | 39 | 13 | ADT91289 | Adt91289 Fe-hydrog |

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| | 38 | 42 | 93.3 | 39 | 13 | ADT91290 | Adt91290 Fe-hydrog |
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| | 42 | 42 | 93.3 | 1265 | 14 | AEB73389 | Aeb73389 cDNA enco |
| | 43 | 42 | 93.3 | 1544 | 14 | ADZ39228 | Adz39228 Trichomon |
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| | 45 | 42 | 93.3 | 1964 | 14 | ADZ39223 | Adz39223 Desulfovi |
| | 46 | 41 | 91.1 | 39 | 13 | ADT91282 | Adt91282 Fe-hydrog |
| | 47 | 38 | 84.4 | 2439 | 12 | ADQ64951 | Adq64951 Novel hum |
| c | 48 | 37 | 82.2 | 110000 | 11 | ADM27081 | Continuation (15 o |
| | 49 | 36 | 80.0 | 1581 | 14 | ACL72707 | Acl72707 M. xanthu |
| c | 50 | 36 | 80.0 | 3797 | 4 | ABL23648 | Abl23648 Drosophil |
| | 51 | 36 | 80.0 | 11612 | 14 | ACL64518 | Acl64518 M. xanthu |
| | 52 | 35 | 77.8 | 646 | 10 | ADD16022 | Add16022 cDNA (Seq |
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| c | 54 | 35 | 77.8 | 1481 | 13 | ADX46435 | Adx46435 Plant ful |
| | 55 | 35 | 77.8 | 1552 | 10 | ADF14287 | Adf14287 Human end |
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| | 62 | 35 | 77.8 | 7676 | 6 | ABN85383 | Abn85383 Human NOV |
| | 63 | 35 | 77.8 | 7728 | 10 | ADF14280 | Adf14280 Human end |
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| | 66 | 35 | 77.8 | 10183 | 14 | ADY18408 | Adyl8408 DNA encod |
| | 67 | 35 | 77.8 | 14244 | 2 | AAX20501 | Aax20501 Polynucle |
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| c | 69 | 34 | 75.6 | 21 | 15 | AEE87528 | Aee87528 Labeled d |
| | 70 | 34 | 75.6 | 192 | 7 | ADS69205 | Ads69205 Corn seed |
| | 71 | 34 | 75.6 | 370 | 6 | ABK62548 | Abk62548 Rat seque |
| | 72 | 34 | 75.6 | 370 | 10 | ADB50649 | Adb50649 Primary r |
| | 73 | 34 | 75.6 | 370 | 13 | ADV39852 | Adv39852 Rat cardi |
| c | 74 | 34 | 75.6 | 1521 | 4 | ABL17483 | Abl17483 Drosophil |
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| | 77 | 33 | 73.3 | 486 | 5 | AAS78464 | Aas78464 DNA encod |
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| | 84 | 33 | 73.3 | 693 | 11 | ACL34123 | Acl34123 Rice abio |
| | 85 | 33 | 73.3 | 693 | 12 | ADI45688 | Adi45688 Corn isop |
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| c | 87 | 33 | 73.3 | 711 | 6 | ABK73019 | Abk73019 Bacillus |
| | 88 | 33 | 73.3 | 714 | 13 | ADT45463 | Adt45463 Bacterial |
| | 89 | 33 | 73.3 | 716 | 10 | ADD17975 | Add17975 cDNA (Seq |
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| | 93 | 33 | 73.3 | 1169 | 14 | ACL63869 | Acl63869 M. xanthu |
| | 94 | 33 | 73.3 | 1290 | 12 | ADP67804 | Adp67804 Maize G34 |
| | 95 | 33 | 73.3 | 1290 | 14 | ADZ68210 | Adz68210 Transcrip |
| | 96 | 33 | 73.3 | 1290 | 14 | AEA26898 | Aea26898 Stress to |
| | 97 | 33 | 73.3 | 1747 | 4 | AAK51546 | Aak51546 Human pol |
| | 98 | 33 | 73.3 | 2000 | 12 | ADJ41348 | Adj41348 Plant cDN |

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| 99 | 33 | 73.3 | 2400 | 10 | ADE07780 | Ade07780 Novel cod |
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| 103 | 33 | 73.3 | 3556 | 5 | ADL45389 | Adl45389 Human ova |
| 104 | 33 | 73.3 | 6642 | 4 | ABL05270 | Abl05270 Drosophil |
| 105 | 33 | 73.3 | 10992 | 4 | ABL05242 | Abl05242 Drosophil |
| 106 | 33 | 73.3 | 18469 | 14 | ACL64742 | AcL64742 M. xanthu |
| 107 | 33 | 73.3 | 114771 | 12 | ADQ17641 | Adq17641 Human sof |
| 108 | 33 | 73.3 | 133893 | 9 | AAD54538 | Aad54538 Human pho |
| 109 | 32 | 71.1 | 132 | 10 | ABZ41895 | Abz41895 N. gonorr |
| 110 | 32 | 71.1 | 386 | 3 | AAH31027 | Aah31027 Human col |
| 111 | 32 | 71.1 | 438 | 4 | ABZ80675 | Abz80675 Beagle do |
| 112 | 32 | 71.1 | 441 | 6 | AAD37892 | Aad37892 Dog lepti |
| 113 | 32 | 71.1 | 444 | 2 | AAT88901 | Aat88901 DNA encod |
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| c 117 | 32 | 71.1 | 675 | 11 | ACH96246 | Ach96246 Klebsiell |
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| 119 | 32 | 71.1 | 700 | 4 | AAH93278 | Aah93278 Human inf |
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| 125 | 32 | 71.1 | 1645 | 8 | ABX05402 | Abx05402 Human nov |
| c 126 | 32 | 71.1 | 1842 | 11 | ABD06236 | Abd06236 Pseudomon |
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| 133 | 32 | 71.1 | 5398 | 2 | AAQ13284 | Aaq13284 P.denitri |
| c 134 | 32 | 71.1 | 5643 | 2 | AAT09946 | Aat09946 Aspergill |
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ALIGNMENTS

RESULT 1

ADT91297

ID ADT91297 standard; DNA; 39 BP.

XX

AC ADT91297;

SCORE Search Results Details for Application 10763712 and Search Result us-10-763-712b-185.rapbn.

| | | | | |
|----------------------------|--------------------------------------|------------------------------|-----------------------|-----------------------------|
| Score Home | Retrieve Application | SCORE System | SCORE | Comments / |
| Page | List | Overview | FAQ | Suggestions |

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OM protein - protein search, using sw model

Run on: June 29, 2006, 08:32:53 ; Search time 16 Seconds
(without alignments)
23.620 Million cell updates/sec

Title: US-10-763-712B-185
Perfect score: 45
Sequence: 1 XXXFXXXGGVMEAAXR 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

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Total number of hits satisfying chosen parameters: 103426

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 5 | 29 | 64.4 | 205 | 6 | US-10-953-349-15317 | Sequence 15317, A |
| 6 | 29 | 64.4 | 514 | 7 | US-11-316-521-28 | Sequence 28, Appl |
| 7 | 29 | 64.4 | 682 | 6 | US-10-449-902-35729 | Sequence 35729, A |
| 8 | 29 | 64.4 | 682 | 6 | US-10-449-902-55720 | Sequence 55720, A |
| 9 | 28 | 62.2 | 74 | 6 | US-10-449-902-42212 | Sequence 42212, A |
| 10 | 28 | 62.2 | 146 | 7 | US-11-055-093-225 | Sequence 225, App |
| 11 | 28 | 62.2 | 166 | 7 | US-11-055-093-155 | Sequence 155, App |
| 12 | 28 | 62.2 | 167 | 7 | US-11-055-093-56 | Sequence 56, Appl |
| 13 | 28 | 62.2 | 167 | 7 | US-11-055-093-151 | Sequence 151, App |
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ALIGNMENTS

RESULT 1

US-10-449-902-46695

; Sequence 46695, Application US/10449902

; Publication No. US20060123505A1

; GENERAL INFORMATION:

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; APPLICANT: Bio-oriented Technology Research Advancement Institution.

; APPLICANT: The Institute of Physical and Chemical Research.

; APPLICANT: Foundation for Advancement of International Science.

; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF

; FILE REFERENCE: MOA-A0205Y1-US

; CURRENT APPLICATION NUMBER: US/10/449,902

; CURRENT FILING DATE: 2003-05-29

; PRIOR APPLICATION NUMBER: JP 2002-203269

; PRIOR FILING DATE: 2002-05-30

; PRIOR APPLICATION NUMBER: JP 2002-383870

; PRIOR FILING DATE: 2002-12-11

; NUMBER OF SEQ ID NOS: 56791

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 46695

; LENGTH: 177

; TYPE: PRT

; ORGANISM: Oryza sativa

US-10-449-902-46695

Query Match 68.9%; Score 31; DB 6; Length 177;

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; Publication No. US20050266541A1

; GENERAL INFORMATION:

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; APPLICANT: Dillon, Harrison F.

; TITLE OF INVENTION: Methods and Compositions for Evolving Microbial Hydrogen

; TITLE OF INVENTION: Production

; FILE REFERENCE: H2042101-CIP

; CURRENT APPLICATION NUMBER: US/10/763,712A

; CURRENT FILING DATE: 2004-01-21

; PRIOR APPLICATION NUMBER: US 10/287,750

; PRIOR FILING DATE: 2002-11-04

; PRIOR APPLICATION NUMBER: US 10/411,910

; PRIOR FILING DATE: 2003-04-12

; PRIOR APPLICATION NUMBER: US 60/500,032

; PRIOR FILING DATE: 2003-09-03

; NUMBER OF SEQ ID NOS: 184

; SOFTWARE: PatentIn version 3.2

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; LENGTH: 19

; TYPE: PRT

; ORGANISM: Artificial sequence

; FEATURE:

; OTHER INFORMATION: Synthetic sequence

US-10-763-712A-130

SCORE Search Results Details for Application 10763712 and Search Result us-10-763-712b 185.ra1.

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OM protein - protein search, using sw model

Run on: June 29, 2006, 08:30:54 ; Search time 48.6667 Seconds
(without alignments)
28.777 Million cell updates/sec

Title: US-10-763-712B-185
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Total number of hits satisfying chosen parameters: 650591

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Post-processing: Minimum Match 0%
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Listing first 150 summaries

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SUMMARIES

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; CURRENT APPLICATION NUMBER: US/10/077,699C
; CURRENT FILING DATE: 2002-02-15
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.2
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US-10-077-699C-6
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RESULT 2

SCORE Search Results Details for Application 10763712 and Search Result us-10-763-712b- 185.rag.

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| Page | List | Overview | FAQ | Suggestions |

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OM protein - protein search, using sw model

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| 27 | 43 | 95.6 | 19 | 9 | AEB73353 | Aeb73353 Segment o |
| 28 | 43 | 95.6 | 19 | 9 | AEB73355 | Aeb73355 Segment o |
| 29 | 43 | 95.6 | 19 | 9 | AEB73351 | Aeb73351 Segment o |
| 30 | 43 | 95.6 | 19 | 9 | AEB73354 | Aeb73354 Segment o |
| 31 | 43 | 95.6 | 19 | 9 | AEB73348 | Aeb73348 Segment o |
| 32 | 43 | 95.6 | 19 | 9 | AEB73341 | Aeb73341 Segment o |
| 33 | 43 | 95.6 | 19 | 9 | AEB73345 | Aeb73345 Segment o |
| 34 | 43 | 95.6 | 19 | 9 | AEB73347 | Aeb73347 Segment o |
| 35 | 43 | 95.6 | 19 | 9 | AEB73350 | Aeb73350 Segment o |
| 36 | 43 | 95.6 | 19 | 9 | AEB73338 | Aeb73338 Segment o |
| 37 | 43 | 95.6 | 25 | 9 | AEB73593 | Aeb73593 Fragment |
| 38 | 43 | 95.6 | 332 | 8 | ADU00337 | Adu00337 Iron hydr |
| 39 | 43 | 95.6 | 332 | 8 | ADU00338 | Adu00338 Iron hydr |
| 40 | 43 | 95.6 | 374 | 8 | ADU00343 | Adu00343 CpI catal |
| 41 | 43 | 95.6 | 386 | 8 | ADU00341 | Adu00341 Iron hydr |
| 42 | 43 | 95.6 | 388 | 8 | ADU00342 | Adu00342 Iron hydr |
| 43 | 43 | 95.6 | 393 | 8 | ADU00340 | Adu00340 Iron hydr |
| 44 | 43 | 95.6 | 403 | 9 | AEB73241 | Aeb73241 Segment o |
| 45 | 43 | 95.6 | 410 | 9 | AEB73299 | Aeb73299 Segment o |
| 46 | 43 | 95.6 | 415 | 9 | AEB73239 | Aeb73239 Segment o |
| 47 | 43 | 95.6 | 436 | 9 | ADY27750 | Ady27750 Chlorella |
| 48 | 43 | 95.6 | 436 | 9 | AEB73219 | Aeb73219 Segment o |
| 49 | 43 | 95.6 | 448 | 9 | ADY27748 | Ady27748 Scenedesm |
| 50 | 43 | 95.6 | 449 | 9 | AEB73297 | Aeb73297 Segment o |
| 51 | 43 | 95.6 | 497 | 9 | ADY27749 | Ady27749 Chlamydom |
| 52 | 43 | 95.6 | 497 | 9 | AEB73305 | Aeb73305 Segment o |
| 53 | 43 | 95.6 | 497 | 9 | AEB73238 | Aeb73238 Segment o |
| 54 | 43 | 95.6 | 505 | 9 | AEB73302 | Aeb73302 Segment o |
| 55 | 43 | 95.6 | 505 | 9 | AEB73303 | Aeb73303 Segment o |
| 56 | 43 | 95.6 | 505 | 9 | AEB73337 | Aeb73337 Gas chann |
| 57 | 43 | 95.6 | 505 | 9 | AEB73240 | Aeb73240 Segment o |

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|-----|----|------|-----|----|----------|----------|-----------|
| 58 | 43 | 95.6 | 554 | 9 | AEB73247 | Aeb73247 | Segment o |
| 59 | 43 | 95.6 | 572 | 9 | AEB73251 | Aeb73251 | Segment o |
| 60 | 43 | 95.6 | 572 | 9 | AEB73324 | Aeb73324 | Segment o |
| 61 | 43 | 95.6 | 572 | 9 | AEB73224 | Aeb73224 | Segment o |
| 62 | 43 | 95.6 | 572 | 9 | AEB73323 | Aeb73323 | Segment o |
| 63 | 43 | 95.6 | 572 | 9 | AEB73225 | Aeb73225 | Segment o |
| 64 | 43 | 95.6 | 574 | 9 | AEB73215 | Aeb73215 | Segment o |
| 65 | 43 | 95.6 | 574 | 9 | AEB73220 | Aeb73220 | Segment o |
| 66 | 43 | 95.6 | 574 | 9 | AEB73316 | Aeb73316 | Segment o |
| 67 | 43 | 95.6 | 578 | 9 | AEB73248 | Aeb73248 | Segment o |
| 68 | 43 | 95.6 | 579 | 9 | AEB73308 | Aeb73308 | Segment o |
| 69 | 43 | 95.6 | 580 | 6 | ABU24770 | Abu24770 | Protein e |
| 70 | 43 | 95.6 | 581 | 9 | AEB73306 | Aeb73306 | Segment o |
| 71 | 43 | 95.6 | 581 | 9 | AEB73242 | Aeb73242 | Segment o |
| 72 | 43 | 95.6 | 582 | 6 | ABU24101 | Abu24101 | Protein e |
| 73 | 43 | 95.6 | 582 | 7 | ADC59546 | Adc59546 | Clostridi |
| 74 | 43 | 95.6 | 582 | 8 | ADR90318 | Adr90318 | Clostridi |
| 75 | 43 | 95.6 | 582 | 9 | AEB73237 | Aeb73237 | Segment o |
| 76 | 43 | 95.6 | 582 | 9 | AEB73315 | Aeb73315 | Segment o |
| 77 | 43 | 95.6 | 588 | 9 | AEB73309 | Aeb73309 | Segment o |
| 78 | 43 | 95.6 | 606 | 9 | AEB73223 | Aeb73223 | Segment o |
| 79 | 43 | 95.6 | 606 | 9 | AEB73300 | Aeb73300 | Segment o |
| 80 | 43 | 95.6 | 606 | 9 | AEB73311 | Aeb73311 | Segment o |
| 81 | 43 | 95.6 | 619 | 9 | AEB73249 | Aeb73249 | Segment o |
| 82 | 42 | 93.3 | 13 | 8 | ADT91230 | Adt91230 | Fe-hydrog |
| 83 | 42 | 93.3 | 13 | 8 | ADT91232 | Adt91232 | Fe-hydrog |
| 84 | 42 | 93.3 | 13 | 8 | ADT91256 | Adt91256 | Fe-hydrog |
| 85 | 42 | 93.3 | 13 | 8 | ADT91258 | Adt91258 | Fe-hydrog |
| 86 | 42 | 93.3 | 13 | 8 | ADT91263 | Adt91263 | Fe-hydrog |
| 87 | 42 | 93.3 | 13 | 8 | ADT91237 | Adt91237 | Fe-hydrog |
| 88 | 42 | 93.3 | 13 | 8 | ADT91240 | Adt91240 | Fe-hydrog |
| 89 | 42 | 93.3 | 13 | 8 | ADT91246 | Adt91246 | Fe-hydrog |
| 90 | 42 | 93.3 | 13 | 8 | ADT91252 | Adt91252 | Fe-hydrog |
| 91 | 42 | 93.3 | 13 | 8 | ADT91226 | Adt91226 | Fe-hydrog |
| 92 | 42 | 93.3 | 13 | 8 | ADT91228 | Adt91228 | Fe-hydrog |
| 93 | 42 | 93.3 | 13 | 8 | ADT91245 | Adt91245 | Fe-hydrog |
| 94 | 42 | 93.3 | 13 | 8 | ADT91234 | Adt91234 | Fe-hydrog |
| 95 | 42 | 93.3 | 13 | 8 | ADT91250 | Adt91250 | Fe-hydrog |
| 96 | 42 | 93.3 | 13 | 8 | ADT91257 | Adt91257 | Fe-hydrog |
| 97 | 42 | 93.3 | 13 | 8 | ADT91264 | Adt91264 | Fe-hydrog |
| 98 | 42 | 93.3 | 13 | 8 | ADT91251 | Adt91251 | Fe-hydrog |
| 99 | 42 | 93.3 | 13 | 8 | ADT91235 | Adt91235 | Fe-hydrog |
| 100 | 42 | 93.3 | 13 | 8 | ADT91233 | Adt91233 | Fe-hydrog |
| 101 | 42 | 93.3 | 13 | 8 | ADT91255 | Adt91255 | Fe-hydrog |
| 102 | 42 | 93.3 | 13 | 8 | ADT91261 | Adt91261 | Fe-hydrog |
| 103 | 42 | 93.3 | 13 | 8 | ADT91265 | Adt91265 | Fe-hydrog |
| 104 | 42 | 93.3 | 13 | 8 | ADT91229 | Adt91229 | Fe-hydrog |
| 105 | 42 | 93.3 | 13 | 8 | ADT91243 | Adt91243 | Fe-hydrog |
| 106 | 42 | 93.3 | 17 | 10 | AEE87521 | Aee87521 | Iron hydr |
| 107 | 42 | 93.3 | 17 | 10 | AEE87522 | Aee87522 | Iron hydr |
| 108 | 42 | 93.3 | 17 | 10 | AEE87524 | Aee87524 | Iron hydr |
| 109 | 42 | 93.3 | 19 | 9 | AEB73349 | Aeb73349 | Segment o |
| 110 | 42 | 93.3 | 19 | 9 | AEB73352 | Aeb73352 | Segment o |
| 111 | 42 | 93.3 | 19 | 9 | AEB73340 | Aeb73340 | Segment o |
| 112 | 42 | 93.3 | 19 | 9 | AEB73343 | Aeb73343 | Segment o |
| 113 | 42 | 93.3 | 19 | 9 | AEB73339 | Aeb73339 | Segment o |
| 114 | 42 | 93.3 | 319 | 8 | ADU00339 | Adu00339 | Iron hydr |
| 115 | 42 | 93.3 | 379 | 9 | AEB73254 | Aeb73254 | Segment o |
| 116 | 42 | 93.3 | 389 | 9 | AEB73245 | Aeb73245 | Segment o |
| 117 | 42 | 93.3 | 421 | 9 | AEB73229 | Aeb73229 | Segment o |
| 118 | 42 | 93.3 | 421 | 9 | AEB73227 | Aeb73227 | Segment o |

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| 119 | 42 | 93.3 | 421 | 9 | AEB73216 | Aeb73216 | Segment o |
| 120 | 42 | 93.3 | 421 | 9 | AEB73255 | Aeb73255 | Segment o |
| 121 | 42 | 93.3 | 421 | 9 | AEB73317 | Aeb73317 | Segment o |
| 122 | 42 | 93.3 | 421 | 9 | AEB73221 | Aeb73221 | Segment o |
| 123 | 42 | 93.3 | 439 | 9 | AEB73253 | Aeb73253 | Segment o |
| 124 | 42 | 93.3 | 449 | 9 | AEB73318 | Aeb73318 | Segment o |
| 125 | 42 | 93.3 | 449 | 9 | AEB73235 | Aeb73235 | Segment o |
| 126 | 42 | 93.3 | 458 | 9 | AEB73246 | Aeb73246 | Segment o |
| 127 | 42 | 93.3 | 468 | 9 | AEB73234 | Aeb73234 | Segment o |
| 128 | 42 | 93.3 | 468 | 9 | AEB73314 | Aeb73314 | Segment o |
| 129 | 42 | 93.3 | 484 | 9 | AEB73226 | Aeb73226 | Segment o |
| 130 | 42 | 93.3 | 555 | 9 | AEB73244 | Aeb73244 | Segment o |
| 131 | 42 | 93.3 | 608 | 9 | AEB73230 | Aeb73230 | Segment o |
| 132 | 42 | 93.3 | 608 | 9 | AEB73304 | Aeb73304 | Segment o |
| 133 | 42 | 93.3 | 636 | 9 | AEB73243 | Aeb73243 | Segment o |
| 134 | 42 | 93.3 | 636 | 9 | AEB73307 | Aeb73307 | Segment o |
| 135 | 42 | 93.3 | 1206 | 9 | AEB73232 | Aeb73232 | Segment o |
| 136 | 42 | 93.3 | 1206 | 9 | AEB73313 | Aeb73313 | Segment o |
| 137 | 41 | 91.1 | 13 | 8 | ADT91247 | Adt91247 | Fe-hydrog |
| 138 | 41 | 91.1 | 13 | 8 | ADT91248 | Adt91248 | Fe-hydrog |
| 139 | 41 | 91.1 | 13 | 8 | ADT91224 | Adt91224 | Fe-hydrog |
| 140 | 41 | 91.1 | 13 | 8 | ADT91239 | Adt91239 | Fe-hydrog |
| 141 | 41 | 91.1 | 13 | 8 | ADT91241 | Adt91241 | Fe-hydrog |
| 142 | 41 | 91.1 | 13 | 8 | ADT91242 | Adt91242 | Fe-hydrog |
| 143 | 41 | 91.1 | 13 | 8 | ADT91249 | Adt91249 | Fe-hydrog |
| 144 | 41 | 91.1 | 13 | 8 | ADT91244 | Adt91244 | Fe-hydrog |
| 145 | 41 | 91.1 | 16 | 9 | AEB73399 | Aeb73399 | Segment o |
| 146 | 40 | 88.9 | 13 | 8 | ADT91238 | Adt91238 | Fe-hydrog |
| 147 | 38 | 84.4 | 9 | 8 | ADT91304 | Adt91304 | Fe-hydrog |
| 148 | 38 | 84.4 | 10 | 9 | ADY27757 | Ady27757 | Iron hydr |
| 149 | 38 | 84.4 | 19 | 9 | AEB73346 | Aeb73346 | Segment o |
| 150 | 38 | 84.4 | 585 | 9 | AEB73228 | Aeb73228 | Segment o |

ALIGNMENTS

RESULT 1

ADT91236

ID ADT91236 standard; peptide; 13 AA.

XX

AC ADT91236;

XX

DT 13-JAN-2005 (first entry)

XX

DE Fe-hydrogenase motif #13.

XX

KW Iron hydrogenase; enzyme.

XX

OS Unidentified.

XX

PN US2004209256-A1.

XX

PD 21-OCT-2004.

XX

PF 12-APR-2003; 2003US-00411910.

XX

PR 12-APR-2003; 2003US-00411910.

XX

PA (SOLA-) SOLAZYME INC.

XX

SCORE Search Results Details for Application 10763712 and Search Result us-10-763-712b-185.rge.

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GenCore version 5.1.9
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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 29, 2006, 19:33:54 ; Search time 4514.67 Seconds
(without alignments)
339.945 Million cell updates/sec

Title: US-10-763-712B-185
Perfect score: 45
Sequence: 1 XXXFXXXGGVMEAAXR 16

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries

Command line parameters:

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-MODEL=frame+_p2n.model -DEV=xlh
-Q=/abss/ABSSWEB_spool/US10763712/runat_29062006_075057_19242/app_query.fasta_1
-DB=GenEmbl -QFMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=150
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=25 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss05h
-USER=US10763712_CCGN_1_1_5767@runat_29062006_075057_19242 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Database : GenEmbl:*
1: gb_env:*

2: gb_pat:*
 3: gb_ph:*
 4: gb_pl:*
 5: gb_pr:*
 6: gb_ro:*
 7: gb_sts:*
 8: gb_sy:*
 9: gb_un:*
 10: gb_vi:*
 11: gb_ov:*
 12: gb_htg:*
 13: gb_in:*
 14: gb_om:*
 15: gb_ba:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query | | DB | ID | Description |
|---------------|-------|-------|--------|----|----------|--------------------|
| | | Match | Length | | | |
| 1 | 45 | 100.0 | 1848 | 13 | AF262401 | AF262401 Trichomon |
| 2 | 43 | 95.6 | 546 | 1 | AY660731 | AY660731 Unculture |
| 3 | 43 | 95.6 | 546 | 1 | AY660732 | AY660732 Unculture |
| 4 | 43 | 95.6 | 546 | 1 | AY660738 | AY660738 Unculture |
| 5 | 43 | 95.6 | 549 | 1 | AY660735 | AY660735 Unculture |
| 6 | 43 | 95.6 | 549 | 1 | AY660736 | AY660736 Unculture |
| 7 | 43 | 95.6 | 654 | 1 | DQ298810 | DQ298810 Unculture |
| 8 | 43 | 95.6 | 654 | 1 | DQ298817 | DQ298817 Unculture |
| 9 | 43 | 95.6 | 654 | 1 | DQ298821 | DQ298821 Unculture |
| 10 | 43 | 95.6 | 654 | 1 | DQ298822 | DQ298822 Unculture |
| 11 | 43 | 95.6 | 654 | 1 | DQ298828 | DQ298828 Unculture |
| 12 | 43 | 95.6 | 657 | 1 | DQ225319 | DQ225319 Unculture |
| 13 | 43 | 95.6 | 657 | 1 | DQ225320 | DQ225320 Unculture |
| 14 | 43 | 95.6 | 657 | 1 | DQ298809 | DQ298809 Unculture |
| 15 | 43 | 95.6 | 657 | 1 | DQ298820 | DQ298820 Unculture |
| 16 | 43 | 95.6 | 663 | 1 | DQ225305 | DQ225305 Unculture |
| 17 | 43 | 95.6 | 663 | 1 | DQ225306 | DQ225306 Unculture |
| 18 | 43 | 95.6 | 663 | 1 | DQ225308 | DQ225308 Unculture |
| 19 | 43 | 95.6 | 663 | 1 | DQ225310 | DQ225310 Unculture |
| 20 | 43 | 95.6 | 663 | 1 | DQ225311 | DQ225311 Unculture |
| 21 | 43 | 95.6 | 663 | 1 | DQ225312 | DQ225312 Unculture |
| 22 | 43 | 95.6 | 663 | 1 | DQ225313 | DQ225313 Unculture |
| 23 | 43 | 95.6 | 663 | 1 | DQ225314 | DQ225314 Unculture |
| 24 | 43 | 95.6 | 663 | 1 | DQ225316 | DQ225316 Unculture |
| 25 | 43 | 95.6 | 663 | 1 | DQ225317 | DQ225317 Unculture |
| 26 | 43 | 95.6 | 663 | 1 | DQ225323 | DQ225323 Unculture |
| 27 | 43 | 95.6 | 663 | 1 | DQ225324 | DQ225324 Unculture |
| 28 | 43 | 95.6 | 663 | 1 | DQ298811 | DQ298811 Unculture |
| 29 | 43 | 95.6 | 663 | 1 | DQ298812 | DQ298812 Unculture |
| 30 | 43 | 95.6 | 663 | 1 | DQ298813 | DQ298813 Unculture |
| 31 | 43 | 95.6 | 663 | 1 | DQ298814 | DQ298814 Unculture |
| 32 | 43 | 95.6 | 663 | 1 | DQ298823 | DQ298823 Unculture |
| 33 | 43 | 95.6 | 663 | 1 | DQ298824 | DQ298824 Unculture |
| 34 | 43 | 95.6 | 663 | 1 | DQ298825 | DQ298825 Unculture |
| 35 | 43 | 95.6 | 663 | 1 | DQ298831 | DQ298831 Unculture |
| 36 | 43 | 95.6 | 663 | 1 | DQ298832 | DQ298832 Unculture |
| 37 | 43 | 95.6 | 667 | 1 | DQ225318 | DQ225318 Unculture |

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| 38 | 43 | 95.6 | 696 | 15 | AY652729 | AY652729 Clostridi |
| 39 | 43 | 95.6 | 696 | 15 | AY652730 | AY652730 Clostridi |
| 40 | 43 | 95.6 | 1041 | 15 | DQ177326 | DQ177326 Ethanolog |
| 41 | 43 | 95.6 | 1518 | 4 | AY436606 | AY436606 Chlamydom |
| 42 | 43 | 95.6 | 1607 | 4 | AF276706 | AF276706 Scenedesm |
| 43 | 43 | 95.6 | 1831 | 15 | AB016820 | AB016820 Clostridi |
| 44 | 43 | 95.6 | 1853 | 4 | AY578072 | AY578072 Chlamydom |
| 45 | 43 | 95.6 | 1940 | 15 | DVHYDC | X57838 D.vulgaris |
| 46 | 43 | 95.6 | 2238 | 15 | AF148212 | AF148212 Clostridi |
| 47 | 43 | 95.6 | 2267 | 15 | CAU09760 | U09760 Clostridium |
| 48 | 43 | 95.6 | 2310 | 15 | CLOHDCI | M81737 Clostridium |
| 49 | 43 | 95.6 | 2347 | 15 | AB159510 | AB159510 Clostridi |
| 50 | 43 | 95.6 | 2399 | 2 | AR641147 | AR641147 Sequence |
| 51 | 43 | 95.6 | 2399 | 4 | CRE012098 | AJ012098 Chlamydom |
| 52 | 43 | 95.6 | 2420 | 4 | CFU298228 | AJ298228 Chlorella |
| 53 | 43 | 95.6 | 2421 | 2 | AR641148 | AR641148 Sequence |
| 54 | 43 | 95.6 | 2454 | 4 | AY055755 | AY055755 Chlamydom |
| 55 | 43 | 95.6 | 2522 | 4 | AF289201 | AF289201 Chlamydom |
| 56 | 43 | 95.6 | 2560 | 4 | AY055756 | AY055756 Chlamydom |
| 57 | 43 | 95.6 | 2636 | 2 | AR641146 | AR641146 Sequence |
| 58 | 43 | 95.6 | 2815 | 15 | CAU15277 | U15277 Clostridium |
| 59 | 43 | 95.6 | 3230 | 15 | AB016775 | AB016775 Clostridi |
| 60 | 43 | 95.6 | 3265 | 2 | AR641145 | AR641145 Sequence |
| 61 | 43 | 95.6 | 3265 | 4 | CFU298227 | AJ298227 Chlorella |
| 62 | 43 | 95.6 | 3584 | 4 | AY436607 | AY436607 Chlamydom |
| 63 | 43 | 95.6 | 4622 | 4 | AY090770 | AY090770 Chlamydom |
| 64 | 43 | 95.6 | 5001 | 2 | AR641143 | AR641143 Sequence |
| 65 | 43 | 95.6 | 5001 | 4 | SOB271546 | AJ271546 Scenedesm |
| 66 | 43 | 95.6 | 5208 | 2 | AR641144 | AR641144 Sequence |
| 67 | 43 | 95.6 | 5999 | 4 | CRE308413 | AJ308413 Chlamydom |
| 68 | 43 | 95.6 | 9033 | 15 | AB035092 | AB035092 Clostridi |
| 69 | 43 | 95.6 | 11577 | 15 | AE013056 | AE013056 Thermoana |
| 70 | 43 | 95.6 | 16133 | 15 | EAC312124 | AJ312124 Eubacteri |
| c 71 | 43 | 95.6 | 66135 | 15 | AP006840_35 | Continuation (36 o |
| c 72 | 43 | 95.6 | 110000 | 15 | AE001437_00 | AE001437 Clostridi |
| c 73 | 43 | 95.6 | 110000 | 15 | CP000142_29 | Continuation (30 o |
| c 74 | 43 | 95.6 | 110000 | 15 | CP000232_17 | Continuation (18 o |
| c 75 | 43 | 95.6 | 110000 | 15 | CP000252_11 | Continuation (12 o |
| c 76 | 43 | 95.6 | 110000 | 15 | CR522870_04 | Continuation (5 of |
| c 77 | 43 | 95.6 | 110000 | 15 | CR522870_05 | Continuation (6 of |
| 78 | 43 | 95.6 | 110000 | 15 | AE014299_40 | Continuation (41 o |
| c 79 | 43 | 95.6 | 110000 | 15 | AE015928_01 | Continuation (2 of |
| c 80 | 43 | 95.6 | 110000 | 15 | AE017226_16 | Continuation (17 o |
| c 81 | 43 | 95.6 | 110000 | 15 | AE017285_18 | Continuation (19 o |
| 82 | 43 | 95.6 | 110000 | 15 | AJ965256_01 | Continuation (2 of |
| 83 | 43 | 95.6 | 110000 | 15 | AP006840_34 | Continuation (35 o |
| c 84 | 43 | 95.6 | 110000 | 15 | BA000016_26 | Continuation (27 o |
| c 85 | 43 | 95.6 | 110000 | 15 | BA000016_27 | Continuation (28 o |
| 86 | 43 | 95.6 | 110000 | 15 | CP000027_01 | Continuation (2 of |
| c 87 | 43 | 95.6 | 349315 | 15 | BX572593 | BX572593 Rhodopseu |
| 88 | 42 | 93.3 | 546 | 1 | AY660733 | AY660733 Unculture |
| 89 | 42 | 93.3 | 546 | 1 | AY660734 | AY660734 Unculture |
| 90 | 42 | 93.3 | 660 | 1 | DQ225309 | DQ225309 Unculture |
| 91 | 42 | 93.3 | 660 | 1 | DQ225315 | DQ225315 Unculture |
| 92 | 42 | 93.3 | 660 | 1 | DQ225322 | DQ225322 Unculture |
| 93 | 42 | 93.3 | 660 | 1 | DQ298807 | DQ298807 Unculture |
| 94 | 42 | 93.3 | 660 | 1 | DQ298808 | DQ298808 Unculture |
| 95 | 42 | 93.3 | 660 | 1 | DQ298818 | DQ298818 Unculture |
| 96 | 42 | 93.3 | 660 | 1 | DQ298819 | DQ298819 Unculture |
| 97 | 42 | 93.3 | 660 | 1 | DQ298829 | DQ298829 Unculture |
| 98 | 42 | 93.3 | 690 | 1 | DQ225307 | DQ225307 Unculture |

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| 99 | 42 | 93.3 | 690 | 1 | DQ225321 | DQ225321 Unculture |
| 100 | 42 | 93.3 | 690 | 1 | DQ298815 | DQ298815 Unculture |
| 101 | 42 | 93.3 | 690 | 1 | DQ298827 | DQ298827 Unculture |
| 102 | 42 | 93.3 | 690 | 1 | DQ298830 | DQ298830 Unculture |
| 103 | 42 | 93.3 | 1337 | 4 | AF516683 | AF516683 Neocallim |
| 104 | 42 | 93.3 | 1544 | 2 | CS073824 | CS073824 Sequence |
| 105 | 42 | 93.3 | 1544 | 13 | TVU19897 | U19897 Trichomonas |
| 106 | 42 | 93.3 | 1659 | 13 | TVU26964 | U26964 Trichomonas |
| 107 | 42 | 93.3 | 1761 | 4 | AF446076 | AF446076 Piromyces |
| 108 | 42 | 93.3 | 1800 | 2 | CS073820 | CS073820 Sequence |
| 109 | 42 | 93.3 | 1800 | 15 | AF331719 | AF331719 Desulfovi |
| 110 | 42 | 93.3 | 1964 | 2 | CS073819 | CS073819 Sequence |
| 111 | 42 | 93.3 | 1964 | 15 | DVUHYDFE | M27212 D.vulgaris |
| 112 | 42 | 93.3 | 2067 | 15 | DVHYDG | X02416 Desulfovibr |
| 113 | 42 | 93.3 | 2467 | 4 | AY033895 | AY033895 Neocallim |
| 114 | 42 | 93.3 | 2585 | 15 | AF120457 | AF120457 Megasphe |
| 115 | 42 | 93.3 | 2887 | 15 | DFHYDABG | Y11759 D.fructosov |
| 116 | 42 | 93.3 | 3625 | 13 | NYHYDROG | Y16775 Nyctotherus |
| 117 | 42 | 93.3 | 3933 | 13 | AY608627 | AY608627 Nyctother |
| 118 | 42 | 93.3 | 110000 | 15 | AE000512_02 | Continuation (3 of |
| 119 | 42 | 93.3 | 110000 | 15 | CP000112_00 | CP000112 Desulfovi |
| 120 | 42 | 93.3 | 110000 | 15 | CP000112_04 | Continuation (5 of |
| c 121 | 42 | 93.3 | 110000 | 15 | CP000112_22 | Continuation (23 o |
| c 122 | 42 | 93.3 | 110000 | 15 | CP000112_23 | Continuation (24 o |
| c 123 | 42 | 93.3 | 110000 | 15 | CP000142_18 | Continuation (19 o |
| c 124 | 42 | 93.3 | 110000 | 15 | CP000142_19 | Continuation (20 o |
| 125 | 42 | 93.3 | 110000 | 15 | AE017285_18 | Continuation (19 o |
| 126 | 40 | 88.9 | 663 | 1 | DQ298826 | DQ298826 Unculture |
| 127 | 39 | 86.7 | 546 | 1 | AY660730 | AY660730 Unculture |
| 128 | 39 | 86.7 | 714 | 15 | AY652731 | AY652731 Clostridi |
| 129 | 39 | 86.7 | 714 | 15 | AY652732 | AY652732 Clostridi |
| 130 | 39 | 86.7 | 110000 | 15 | BX571966_03 | Continuation (4 of |
| c 131 | 39 | 86.7 | 110000 | 15 | CP000011_19 | Continuation (20 o |
| 132 | 38 | 84.4 | 662 | 7 | BV412230 | BV412230 S229P6283 |
| 133 | 38 | 84.4 | 2439 | 2 | CQ843465 | CQ843465 Sequence |
| 134 | 38 | 84.4 | 2439 | 5 | AK126441 | AK126441 Homo sapi |
| 135 | 38 | 84.4 | 5251 | 15 | DFU07229 | U07229 Desulfovibr |
| 136 | 38 | 84.4 | 68326 | 5 | AC011283 | AC011283 Homo sapi |
| 137 | 38 | 84.4 | 110000 | 15 | CP000142_18 | Continuation (19 o |
| c 138 | 38 | 84.4 | 110000 | 15 | AE017221_14 | Continuation (15 o |
| 139 | 38 | 84.4 | 167348 | 12 | AC013782 | AC013782 Homo sapi |
| 140 | 38 | 84.4 | 173960 | 5 | AC093885 | AC093885 Homo sapi |
| c 141 | 37 | 82.2 | 11722 | 15 | AE010432 | AE010432 Methanopy |
| 142 | 37 | 82.2 | 68100 | 4 | AFA14E5 | AL683874 Aspergill |
| c 143 | 37 | 82.2 | 89888 | 12 | AY294423_3 | Continuation (4 of |
| c 144 | 37 | 82.2 | 110000 | 15 | AJ965256_04 | Continuation (5 of |
| c 145 | 37 | 82.2 | 110000 | 15 | CP000027_05 | Continuation (6 of |
| 146 | 37 | 82.2 | 141756 | 5 | AL355382 | AL355382 Human DNA |
| c 147 | 37 | 82.2 | 158483 | 12 | AC015548 | AC015548 Homo sapi |
| 148 | 37 | 82.2 | 161371 | 6 | AC132590 | AC132590 Mus muscu |
| 149 | 37 | 82.2 | 193170 | 12 | AC068652 | AC068652 Mus muscu |
| c 150 | 37 | 82.2 | 200472 | 6 | AC162035 | AC162035 Mus muscu |

ALIGNMENTS

RESULT 1

AF262401

LOCUS AF262401 1848 bp mRNA linear INV 09-NOV-2000

DEFINITION Trichomonas vaginalis putative 64kDa iron hydrogenase mRNA, partial cds.

2: gb_est3:*
 3: gb_est4:*
 4: gb_est5:*
 5: gb_est6:*
 6: gb_hlc:*
 7: gb_est2:*
 8: gb_est7:*
 9: gb_est8:*
 10: gb_est9:*
 11: gb_gss1:*
 12: gb_gss2:*
 13: gb_gss3:*
 14: gb_gss4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result | No. | Score | % Query Match | Length | DB | ID | Description |
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| | 1 | 45 | 100.0 | 601 | 8 | CV216049 | CV216049 EST875759 |
| c | 2 | 45 | 100.0 | 603 | 8 | CV216048 | CV216048 EST875758 |
| | 3 | 45 | 100.0 | 836 | 8 | CV210634 | CV210634 EST870344 |
| | 4 | 45 | 100.0 | 883 | 8 | CV209967 | CV209967 EST869677 |
| c | 5 | 45 | 100.0 | 973 | 8 | CV209966 | CV209966 EST869676 |
| c | 6 | 45 | 100.0 | 1033 | 8 | CV210633 | CV210633 EST870343 |
| | 7 | 43 | 95.6 | 549 | 7 | BE337478 | BE337478 894046C04 |
| | 8 | 43 | 95.6 | 617 | 2 | BI999849 | BI999849 1031079E0 |
| | 9 | 43 | 95.6 | 644 | 2 | BM003317 | BM003317 1031109G0 |
| | 10 | 43 | 95.6 | 658 | 2 | BI726441 | BI726441 1031085C0 |
| | 11 | 43 | 95.6 | 1050 | 13 | CW918425 | CW918425 EDCA527TR |
| c | 12 | 43 | 95.6 | 1118 | 13 | CW934222 | CW934222 EDCCN13TR |
| | 13 | 38 | 84.4 | 532 | 7 | BE518304 | BE518304 WHE0808_F |
| | 14 | 38 | 84.4 | 563 | 9 | DB270347 | DB270347 DB270347 |
| | 15 | 38 | 84.4 | 563 | 9 | DB277683 | DB277683 DB277683 |
| | 16 | 38 | 84.4 | 564 | 9 | DB277650 | DB277650 DB277650 |
| | 17 | 38 | 84.4 | 616 | 5 | CD878589 | CD878589 AZO4.103C |
| | 18 | 38 | 84.4 | 694 | 5 | CD872019 | CD872019 AZO2.119K |
| | 19 | 38 | 84.4 | 758 | 4 | CB336646 | CB336646 Tc021E12F |
| | 20 | 38 | 84.4 | 951 | 2 | BG539706 | BG539706 602567670 |
| c | 21 | 37 | 82.2 | 532 | 2 | BG098351 | BG098351 EST462870 |
| | 22 | 37 | 82.2 | 592 | 4 | CA006652 | CA006652 HU05F03r |
| c | 23 | 37 | 82.2 | 698 | 10 | DV155376 | DV155376 CV03097B2 |
| | 24 | 36 | 80.0 | 221 | 13 | CZ487899 | CZ487899 f05264-5p |
| c | 25 | 36 | 80.0 | 352 | 4 | BY048856 | BY048856 BY048856 |
| | 26 | 36 | 80.0 | 361 | 11 | AQ462547 | AQ462547 HS_5213_A |
| c | 27 | 36 | 80.0 | 429 | 1 | AU078680 | AU078680 AU078680 |
| c | 28 | 36 | 80.0 | 610 | 7 | BF490206 | BF490206 AT26517.5 |
| c | 29 | 36 | 80.0 | 636 | 4 | CB647679 | CB647679 OSJNEb10L |
| c | 30 | 36 | 80.0 | 687 | 7 | BF498871 | BF498871 AT13281.5 |
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| c | 32 | 36 | 80.0 | 701 | 7 | BF493192 | BF493192 AT01494.5 |
| c | 33 | 36 | 80.0 | 704 | 7 | BF493667 | BF493667 AT01991.5 |
| c | 34 | 36 | 80.0 | 705 | 7 | BF493579 | BF493579 AT01880.5 |
| c | 35 | 36 | 80.0 | 714 | 4 | CB647837 | CB647837 OSJNEb10P |
| c | 36 | 36 | 80.0 | 730 | 7 | BF506037 | BF506037 AT08391.5 |
| c | 37 | 36 | 80.0 | 1022 | 3 | BQ714256 | BQ714256 AGENCOURT |
| c | 38 | 35 | 77.8 | 298 | 2 | BI059695 | BI059695 MR4-UT005 |

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|---|----|----|------|-----|----|----------|---------------------|
| c | 39 | 35 | 77.8 | 318 | 5 | CI285736 | CI285736 CI285736 |
| | 40 | 35 | 77.8 | 344 | 4 | C28416 | C28416 C28416 Rice |
| c | 41 | 35 | 77.8 | 362 | 10 | DV168716 | DV168716 ZM_BFb016 |
| | 42 | 35 | 77.8 | 367 | 11 | AZ920964 | AZ920964 1006023A0 |
| | 43 | 35 | 77.8 | 372 | 5 | CI291090 | CI291090 CI291090 |
| | 44 | 35 | 77.8 | 377 | 9 | DN999534 | DN999534 TC104360 |
| | 45 | 35 | 77.8 | 383 | 8 | CV723806 | CV723806 root--04- |
| | 46 | 35 | 77.8 | 392 | 5 | CF990916 | CF990916 18317rsic |
| c | 47 | 35 | 77.8 | 405 | 4 | BY308010 | BY308010 BY308010 |
| c | 48 | 35 | 77.8 | 425 | 9 | DN141900 | DN141900 5036_D03_ |
| c | 49 | 35 | 77.8 | 429 | 5 | CI296013 | CI296013 CI296013 |
| | 50 | 35 | 77.8 | 442 | 7 | BF040679 | BF040679 BP250002A |
| c | 51 | 35 | 77.8 | 454 | 12 | CC032111 | CC032111 3591_1_12 |
| | 52 | 35 | 77.8 | 459 | 5 | CF984650 | CF984650 15258rsic |
| | 53 | 35 | 77.8 | 470 | 5 | CI309180 | CI309180 CI309180 |
| | 54 | 35 | 77.8 | 472 | 9 | DN106393 | DN106393 1103768 M |
| | 55 | 35 | 77.8 | 475 | 4 | BY158321 | BY158321 BY158321 |
| c | 56 | 35 | 77.8 | 489 | 12 | CC020874 | CC020874 3591_1_21 |
| c | 57 | 35 | 77.8 | 499 | 8 | CO532607 | CO532607 3530_1_21 |
| | 58 | 35 | 77.8 | 500 | 5 | CF984527 | CF984527 17633rsic |
| | 59 | 35 | 77.8 | 514 | 14 | CT105399 | CT105399 Sus scrof |
| | 60 | 35 | 77.8 | 532 | 5 | CF990543 | CF990543 17881rsic |
| | 61 | 35 | 77.8 | 534 | 7 | BF044803 | BF044803 BP250019A |
| | 62 | 35 | 77.8 | 537 | 10 | DW992503 | DW992503 EST44884 |
| c | 63 | 35 | 77.8 | 549 | 10 | DV535776 | DV535776 ZM_BFb022 |
| | 64 | 35 | 77.8 | 554 | 9 | DA622709 | DA622709 DA622709 |
| c | 65 | 35 | 77.8 | 573 | 10 | DR808400 | DR808400 ZM_BFb003 |
| c | 66 | 35 | 77.8 | 579 | 2 | BF913740 | BF913740 MR4-UT005 |
| c | 67 | 35 | 77.8 | 580 | 8 | CV663568 | CV663568 LCPE04EX0 |
| c | 68 | 35 | 77.8 | 586 | 10 | DV513661 | DV513661 ZM_BFb019 |
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| c | 70 | 35 | 77.8 | 588 | 13 | CZ555896 | CZ555896 M0029301 |
| | 71 | 35 | 77.8 | 598 | 7 | BF380280 | BF380280 MR4-UT005 |
| c | 72 | 35 | 77.8 | 604 | 14 | CNS04032 | AL268391 Tetraodon |
| | 73 | 35 | 77.8 | 605 | 10 | DW552619 | DW552619 EST_ss1_ |
| c | 74 | 35 | 77.8 | 611 | 10 | DV541347 | DV541347 ZM_BFb023 |
| | 75 | 35 | 77.8 | 621 | 2 | BG573944 | BG573944 602593393 |
| c | 76 | 35 | 77.8 | 639 | 12 | CG351362 | CG351362 OGXAN07TH |
| | 77 | 35 | 77.8 | 642 | 14 | DX272345 | DX272345 OR_ABa016 |
| | 78 | 35 | 77.8 | 646 | 4 | CA758423 | CA758423 BR0500150 |
| | 79 | 35 | 77.8 | 650 | 5 | CI136609 | CI136609 CI136609 |
| | 80 | 35 | 77.8 | 650 | 5 | CI138269 | CI138269 CI138269 |
| c | 81 | 35 | 77.8 | 655 | 5 | CD216274 | CD216274 pgp2n.pk0 |
| c | 82 | 35 | 77.8 | 656 | 12 | CG288985 | CG288985 OG1BD33TV |
| c | 83 | 35 | 77.8 | 666 | 10 | DV536364 | DV536364 ZM_BFb022 |
| c | 84 | 35 | 77.8 | 672 | 4 | CA194351 | CA194351 SCRFBSB102 |
| | 85 | 35 | 77.8 | 674 | 13 | CL611557 | CL611557 OR_BB000 |
| c | 86 | 35 | 77.8 | 675 | 10 | DT641459 | DT641459 ZM_BFb009 |
| c | 87 | 35 | 77.8 | 681 | 10 | DV030843 | DV030843 ZM_BFb015 |
| | 88 | 35 | 77.8 | 700 | 5 | CI138741 | CI138741 CI138741 |
| | 89 | 35 | 77.8 | 700 | 5 | CI255938 | CI255938 CI255938 |
| | 90 | 35 | 77.8 | 700 | 5 | CI256212 | CI256212 CI256212 |
| c | 91 | 35 | 77.8 | 700 | 14 | AG108792 | AG108792 Pan trogl |
| c | 92 | 35 | 77.8 | 721 | 10 | DV532539 | DV532539 ZM_BFb022 |
| c | 93 | 35 | 77.8 | 725 | 4 | CB644939 | CB644939 OSJNEb06F |
| c | 94 | 35 | 77.8 | 728 | 4 | CB651572 | CB651572 OSJNEb16J |
| c | 95 | 35 | 77.8 | 731 | 4 | CB642456 | CB642456 OSJNEb02K |
| c | 96 | 35 | 77.8 | 740 | 3 | BU106381 | BU106381 603007091 |
| | 97 | 35 | 77.8 | 741 | 4 | CB653991 | CB653991 OSJNEc05I |
| c | 98 | 35 | 77.8 | 745 | 4 | CB642552 | CB642552 OSJNEb02M |
| c | 99 | 35 | 77.8 | 747 | 4 | CB653992 | CB653992 OSJNEc05I |

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| c 100 | 35 | 77.8 | 749 | 4 | CB648890 | CB648890 OSJNEb12I |
| c 101 | 35 | 77.8 | 750 | 10 | DV502245 | DV502245 ZM_BFb017 |
| c 102 | 35 | 77.8 | 761 | 5 | CK762050 | CK762050 atr02-7ms |
| c 103 | 35 | 77.8 | 766 | 10 | DR965772 | DR965772 ZM_BFb008 |
| 104 | 35 | 77.8 | 774 | 4 | CB648889 | CB648889 OSJNEb12I |
| c 105 | 35 | 77.8 | 776 | 4 | CB662606 | CB662606 OSJNEd06M |
| c 106 | 35 | 77.8 | 778 | 10 | DV020937 | DV020937 ZM_BFb013 |
| 107 | 35 | 77.8 | 778 | 13 | CL705690 | CL705690 SP_Bb004 |
| c 108 | 35 | 77.8 | 787 | 10 | DR955386 | DR955386 ZM_BFb004 |
| c 109 | 35 | 77.8 | 792 | 10 | DR814011 | DR814011 ZM_BFb004 |
| 110 | 35 | 77.8 | 793 | 4 | CB650095 | CB650095 OSJNEb14F |
| c 111 | 35 | 77.8 | 794 | 4 | CB650096 | CB650096 OSJNEb14F |
| c 112 | 35 | 77.8 | 803 | 10 | DR814506 | DR814506 ZM_BFb004 |
| 113 | 35 | 77.8 | 806 | 4 | CB642455 | CB642455 OSJNEb02K |
| 114 | 35 | 77.8 | 815 | 4 | CB651571 | CB651571 OSJNEb16J |
| 115 | 35 | 77.8 | 819 | 4 | CB651570 | CB651570 OSJNEb16J |
| c 116 | 35 | 77.8 | 819 | 10 | DR970188 | DR970188 ZM_BFb009 |
| 117 | 35 | 77.8 | 825 | 4 | CB645740 | CB645740 OSJNEb07K |
| c 118 | 35 | 77.8 | 826 | 10 | DR811791 | DR811791 ZM_BFb004 |
| c 119 | 35 | 77.8 | 827 | 10 | DT942309 | DT942309 ZM_BFb012 |
| c 120 | 35 | 77.8 | 837 | 4 | CB645741 | CB645741 OSJNEb07K |
| 121 | 35 | 77.8 | 845 | 4 | CB677558 | CB677558 OSJNEe14K |
| 122 | 35 | 77.8 | 846 | 4 | CB642551 | CB642551 OSJNEb02M |
| 123 | 35 | 77.8 | 875 | 12 | BZ652401 | BZ652401 OGCCW45TC |
| c 124 | 35 | 77.8 | 879 | 10 | DR819123 | DR819123 ZM_BFb005 |
| 125 | 35 | 77.8 | 890 | 4 | CB644938 | CB644938 OSJNEb06F |
| c 126 | 35 | 77.8 | 906 | 13 | CL461908 | CL461908 SAIL_1154 |
| c 127 | 35 | 77.8 | 909 | 10 | DR964150 | DR964150 ZM_BFb008 |
| 128 | 35 | 77.8 | 914 | 8 | CV089450 | CV089450 est_c_vir |
| 129 | 35 | 77.8 | 944 | 12 | CG288361 | CG288361 OGXCM32TH |
| c 130 | 35 | 77.8 | 1010 | 14 | CNS03T9C | AL259545 Tetraodon |
| c 131 | 35 | 77.8 | 1029 | 13 | CW923845 | CW923845 EDCB082TR |
| 132 | 35 | 77.8 | 1098 | 14 | CNS03BCR | AL236340 Tetraodon |
| c 133 | 35 | 77.8 | 1109 | 2 | BG110233 | BG110233 602279886 |
| 134 | 35 | 77.8 | 1200 | 8 | CX099889 | CX099889 RECM0658 |
| 135 | 35 | 77.8 | 1952 | 6 | BC018692 | BC018692 Homo sapi |
| c 136 | 34 | 75.6 | 122 | 12 | BZ596952 | BZ596952 SALK_0979 |
| 137 | 34 | 75.6 | 195 | 5 | CF558658 | CF558658 1115039G1 |
| 138 | 34 | 75.6 | 234 | 7 | AW433603 | AW433603 UI-R-BJ0p |
| 139 | 34 | 75.6 | 274 | 2 | BG183978 | BG183978 RST2893 A |
| 140 | 34 | 75.6 | 300 | 1 | AU115507 | AU115507 AU115507 |
| 141 | 34 | 75.6 | 301 | 5 | CK783132 | CK783132 UI-D-GC1- |
| c 142 | 34 | 75.6 | 306 | 14 | DX255468 | DX255468 OR_ABa014 |
| 143 | 34 | 75.6 | 310 | 7 | AW532409 | AW532409 UI-R-BS0- |
| 144 | 34 | 75.6 | 311 | 1 | AI714009 | AI714009 UI-R-AF1- |
| 145 | 34 | 75.6 | 331 | 8 | CR463215 | CR463215 CR463215 |
| 146 | 34 | 75.6 | 338 | 1 | AI010046 | AI010046 EST204497 |
| c 147 | 34 | 75.6 | 360 | 4 | C68144 | C68144 C68144 Yuji |
| 148 | 34 | 75.6 | 370 | 1 | AA997765 | AA997765 UI-R-C0-h |
| 149 | 34 | 75.6 | 373 | 7 | BE105797 | BE105797 UI-R-BX0- |
| 150 | 34 | 75.6 | 381 | 7 | AW253518 | AW253518 UI-R-BJ0- |

ALIGNMENTS

RESULT 1
CV216049
LOCUS CV216049 601 bp mRNA linear EST 16-SEP-2004
DEFINITION EST875759 non-normalized T1 cDNA library Trichomonas vaginalis cDNA
clone TVTCC29 5' end, mRNA sequence.
ACCESSION CV216049

SCORE Search Results Details for Application 10763712 and Search Result us-10-763-712b-186.rst.

| | | | | |
|----------------------------|--------------------------------------|------------------------------|-----------------------|-----------------------------|
| Score Home | Retrieve Application | SCORE System | SCORE | Comments / |
| Page | List | Overview | FAQ | Suggestions |

This page gives you Search Results detail for the Application 10763712 and Search Result us-10-763-712b-186.rst.

start

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GenCore version 5.1.9
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OM protein - nucleic search, using frame plus p2n model

```
Run on:      June 29, 2006, 19:47:05 ; Search time 2471.33 Seconds
              (without alignments)
              271.526 Million cell updates/sec
```

Title: US-10-763-712B-186
Perfect score: 29
Sequence: 1 ADXTIXEE 8

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Scoring table:  BLOSUM62
                  Xgapop 10.0 , Xgapext 0.5
                  Ygapop 10.0 , Ygapext 0.5
                  Fgapop  6.0 , Fgapext 7.0
                  Delop  6.0 , Delext  7.0
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Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 150 summaries
```

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Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlp
-Q=/abss/ABSSWEB_spool/US10763712/runat_29062006_075100_19328/app_query.fasta_1
-DB=EST -QFMT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=150
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=25 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss03p
-USER=US10763712_@CGN_1_1_12067_@runat_29062006_075100_19328 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
```

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Database :      EST:*
           1:    qb est1:*
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2: gb_est3:*
 3: gb_est4:*
 4: gb_est5:*
 5: gb_est6:*
 6: gb_hlc:*
 7: gb_est2:*
 8: gb_est7:*
 9: gb_est8:*
 10: gb_est9:*
 11: gb_gss1:*
 12: gb_gss2:*
 13: gb_gss3:*
 14: gb_gss4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result | No. | Score | % Query Match | Length | DB | ID | Description |
|--------|-----|-------|---------------------|--------|----|----------|--------------------|
| | 1 | 29 | 100.0 | 439 | 1 | AA802002 | AA802002 GM03708.5 |
| | 2 | 29 | 100.0 | 512 | 10 | DR446627 | DR446627 AR1034D02 |
| | 3 | 29 | 100.0 | 600 | 11 | AZ440534 | AZ440534 1M0231F12 |
| | 4 | 29 | 100.0 | 620 | 1 | AI114013 | AI114013 GH10644.5 |
| c | 5 | 29 | 100.0 | 799 | 13 | CL664979 | CL664979 PRI0148c_ |
| | 6 | 28 | 96.6 | 308 | 1 | AV119417 | AV119417 AV119417 |
| c | 7 | 28 | 96.6 | 358 | 11 | AQ763009 | AQ763009 HS_3191_B |
| | 8 | 28 | 96.6 | 392 | 4 | CB376953 | CB376953 Hb02A08 L |
| c | 9 | 28 | 96.6 | 399 | 1 | AI985747 | AI985747 wr76h02.x |
| | 10 | 28 | 96.6 | 400 | 4 | CB546520 | CB546520 AMGNNUC:N |
| c | 11 | 28 | 96.6 | 404 | 11 | AZ929796 | AZ929796 479.dil55 |
| | 12 | 28 | 96.6 | 424 | 10 | DY181351 | DY181351 000217BOV |
| | 13 | 28 | 96.6 | 451 | 10 | DW207354 | DW207354 EST23618 |
| | 14 | 28 | 96.6 | 494 | 2 | BM522129 | BM522129 ESSU0666 |
| c | 15 | 28 | 96.6 | 508 | 13 | CZ769915 | CZ769915 OC__Ba012 |
| c | 16 | 28 | 96.6 | 520 | 11 | AQ853247 | AQ853247 LMAJFV1_1 |
| | 17 | 28 | 96.6 | 545 | 10 | DW210560 | DW210560 EST26824 |
| | 18 | 28 | 96.6 | 548 | 12 | CE712029 | CE712029 tigr-gss- |
| | 19 | 28 | 96.6 | 549 | 1 | AU199321 | AU199321 AU199321 |
| c | 20 | 28 | 96.6 | 553 | 10 | DR507779 | DR507779 WS02720.B |
| | 21 | 28 | 96.6 | 558 | 10 | DW205650 | DW205650 EST21914 |
| | 22 | 28 | 96.6 | 577 | 10 | DW206113 | DW206113 EST22377 |
| c | 23 | 28 | 96.6 | 579 | 10 | DW992636 | DW992636 EST45017 |
| | 24 | 28 | 96.6 | 584 | 8 | CV244922 | CV244922 WS0255.B2 |
| c | 25 | 28 | 96.6 | 586 | 14 | AG211417 | AG211417 Oryza sat |
| | 26 | 28 | 96.6 | 595 | 10 | DW201862 | DW201862 EST18132 |
| | 27 | 28 | 96.6 | 600 | 5 | CD352191 | CD352191 UI-M-GI0- |
| | 28 | 28 | 96.6 | 601 | 5 | CK391979 | CK391979 K0839C03- |
| | 29 | 28 | 96.6 | 611 | 1 | AU206495 | AU206495 AU206495 |
| | 30 | 28 | 96.6 | 618 | 9 | DR028491 | DR028491 bda010051 |
| c | 31 | 28 | 96.6 | 621 | 11 | AQ999205 | AQ999205 RPCI-23-3 |
| c | 32 | 28 | 96.6 | 629 | 11 | AQ047901 | AQ047901 cLM-4a8-u |
| | 33 | 28 | 96.6 | 630 | 7 | AW753457 | AW753457 QV2-CT026 |
| | 34 | 28 | 96.6 | 631 | 1 | AU205723 | AU205723 AU205723 |
| | 35 | 28 | 96.6 | 631 | 8 | CV223829 | CV223829 CS_hyp_08 |
| | 36 | 28 | 96.6 | 632 | 14 | CT287874 | CT287874 Sus scrof |
| | 37 | 28 | 96.6 | 634 | 5 | CK617072 | CK617072 mk01a05.y |
| c | 38 | 28 | 96.6 | 639 | 8 | CX173957 | CX173957 B11_69-10 |

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| | 39 | 28 | 96.6 | 641 | 13 | CW482884 | CW482884 fsbb001f2 |
| c | 40 | 28 | 96.6 | 654 | 13 | CW482883 | CW482883 fsbb001f2 |
| | 41 | 28 | 96.6 | 664 | 12 | CE068236 | CE068236 tigr-gss- |
| | 42 | 28 | 96.6 | 668 | 12 | CC946162 | CC946162 BOIFG75TF |
| | 43 | 28 | 96.6 | 671 | 10 | DW212585 | DW212585 EST28849 |
| c | 44 | 28 | 96.6 | 675 | 5 | CF306407 | CF306407 HDA1--03- |
| | 45 | 28 | 96.6 | 677 | 10 | DR525776 | DR525776 WS02720.B |
| | 46 | 28 | 96.6 | 678 | 10 | DW219177 | DW219177 EST35435 |
| c | 47 | 28 | 96.6 | 689 | 14 | CR060167 | CR060167 Forward s |
| | 48 | 28 | 96.6 | 692 | 12 | CE507471 | CE507471 tigr-gss- |
| | 49 | 28 | 96.6 | 694 | 8 | CN359881 | CN359881 170005315 |
| c | 50 | 28 | 96.6 | 700 | 8 | CR373248 | CR373248 CR373248 |
| c | 51 | 28 | 96.6 | 702 | 11 | BH925823 | BH925823 odi59c04. |
| c | 52 | 28 | 96.6 | 703 | 11 | BH651871 | BH651871 BOHYA03TR |
| | 53 | 28 | 96.6 | 708 | 13 | CW519540 | CW519540 OP__Ba002 |
| | 54 | 28 | 96.6 | 712 | 2 | BI107985 | BI107985 602902361 |
| c | 55 | 28 | 96.6 | 714 | 11 | BH923230 | BH923230 odi01h09. |
| | 56 | 28 | 96.6 | 728 | 14 | AG424374 | AG424374 Mus muscu |
| | 57 | 28 | 96.6 | 744 | 14 | AG441044 | AG441044 Mus muscu |
| | 58 | 28 | 96.6 | 746 | 11 | AZ133410 | AZ133410 OSJNBb010 |
| | 59 | 28 | 96.6 | 754 | 8 | CO247598 | CO247598 AGENCOURT |
| | 60 | 28 | 96.6 | 757 | 8 | CR284966 | CR284966 CR284966 |
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| | 62 | 28 | 96.6 | 759 | 14 | AG424375 | AG424375 Mus muscu |
| | 63 | 28 | 96.6 | 770 | 10 | DR523819 | DR523819 WS02715.B |
| | 64 | 28 | 96.6 | 782 | 2 | BI665663 | BI665663 603289659 |
| c | 65 | 28 | 96.6 | 784 | 5 | CF817640 | CF817640 EST695022 |
| | 66 | 28 | 96.6 | 786 | 5 | CD656171 | CD656171 AGENCOURT |
| c | 67 | 28 | 96.6 | 789 | 11 | BZ494093 | BZ494093 BONHI51TR |
| | 68 | 28 | 96.6 | 800 | 13 | DU274767 | DU274767 109844800 |
| c | 69 | 28 | 96.6 | 812 | 11 | BH424746 | BH424746 BOGUP64TR |
| | 70 | 28 | 96.6 | 817 | 11 | BH513858 | BH513858 BOGYC15TR |
| | 71 | 28 | 96.6 | 818 | 8 | CV123638 | CV123638 OSTF30015 |
| | 72 | 28 | 96.6 | 823 | 9 | DR029231 | DR029231 bda010072 |
| | 73 | 28 | 96.6 | 828 | 10 | DT489984 | DT489984 WS02543.B |
| | 74 | 28 | 96.6 | 830 | 9 | DR029576 | DR029576 bda010082 |
| | 75 | 28 | 96.6 | 835 | 10 | DR537717 | DR537717 WS02752.C |
| | 76 | 28 | 96.6 | 861 | 10 | DT491462 | DT491462 WS02547.C |
| c | 77 | 28 | 96.6 | 866 | 13 | DU119811 | DU119811 KBrH101B1 |
| c | 78 | 28 | 96.6 | 878 | 14 | CR241993 | CR241993 Forward s |
| | 79 | 28 | 96.6 | 885 | 10 | DT525309 | DT525309 WS02045.C |
| | 80 | 28 | 96.6 | 889 | 13 | DU083509 | DU083509 279791 To |
| | 81 | 28 | 96.6 | 914 | 10 | DT489748 | DT489748 WS02543.B |
| | 82 | 28 | 96.6 | 917 | 3 | BU178367 | BU178367 AGENCOURT |
| | 83 | 28 | 96.6 | 917 | 10 | DT488741 | DT488741 WS02537.B |
| | 84 | 28 | 96.6 | 1005 | 3 | BM564901 | BM564901 AGENCOURT |
| | 85 | 28 | 96.6 | 1082 | 3 | BQ955528 | BQ955528 AGENCOURT |
| c | 86 | 28 | 96.6 | 1473 | 13 | CL647975 | CL647975 CH213-157 |
| | 87 | 28 | 96.6 | 5391 | 14 | DQ037846 | DQ037846 Homo sapi |
| | 88 | 28 | 96.6 | 5391 | 14 | DQ037847 | DQ037847 Pan trogl |
| | 89 | 27 | 93.1 | 145 | 12 | BZ613479 | BZ613479 KBrH13901 |
| c | 90 | 27 | 93.1 | 147 | 1 | AI758327 | AI758327 ty06d05.x |
| | 91 | 27 | 93.1 | 157 | 4 | BX610202 | BX610202 BX610202 |
| | 92 | 27 | 93.1 | 178 | 4 | CA364740 | CA364740 639708 NC |
| | 93 | 27 | 93.1 | 195 | 4 | CB042710 | CB042710 4007513 B |
| c | 94 | 27 | 93.1 | 235 | 1 | AV341479 | AV341479 AV341479 |
| | 95 | 27 | 93.1 | 236 | 11 | AQ586437 | AQ586437 RPCI-11-4 |
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| | 97 | 27 | 93.1 | 281 | 1 | AA682378 | AA682378 zj86b03.s |
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| | 99 | 27 | 93.1 | 288 | 5 | CD966095 | CD966095 SEL_73 Ge |

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| 104 | 27 | 93.1 | 297 | 10 | AF142229 | AF142229 | HIV-1 | fro |
| 105 | 27 | 93.1 | 297 | 10 | AF142231 | AF142231 | HIV-1 | fro |
| 106 | 27 | 93.1 | 297 | 10 | AF142232 | AF142232 | HIV-1 | fro |
| 107 | 27 | 93.1 | 297 | 10 | AF142233 | AF142233 | HIV-1 | fro |
| 108 | 27 | 93.1 | 297 | 10 | AF142234 | AF142234 | HIV-1 | fro |
| 109 | 27 | 93.1 | 297 | 10 | AF142235 | AF142235 | HIV-1 | fro |
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| 111 | 27 | 93.1 | 297 | 10 | AF142238 | AF142238 | HIV-1 | fro |
| 112 | 27 | 93.1 | 297 | 10 | AF142239 | AF142239 | HIV-1 | fro |
| 113 | 27 | 93.1 | 297 | 10 | AF204326 | AF204326 | HIV-1 | pat |
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| 115 | 27 | 93.1 | 297 | 10 | AF227687 | AF227687 | HIV-1 | pat |
| 116 | 27 | 93.1 | 297 | 10 | AF227688 | AF227688 | HIV-1 | pat |
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| 120 | 27 | 93.1 | 297 | 10 | AF311132 | AF311132 | HIV-1 | iso |
| 121 | 27 | 93.1 | 297 | 10 | AF317024 | AF317024 | HIV-1 | GR. |
| 122 | 27 | 93.1 | 297 | 10 | AF544416 | AF544416 | HIV-1 | iso |
| 123 | 27 | 93.1 | 297 | 10 | AF544475 | AF544475 | HIV-1 | iso |
| 124 | 27 | 93.1 | 297 | 10 | AF544509 | AF544509 | HIV-1 | iso |
| 125 | 27 | 93.1 | 297 | 10 | AF544519 | AF544519 | HIV-1 | iso |
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| 128 | 27 | 93.1 | 297 | 10 | AF544560 | AF544560 | HIV-1 | iso |
| 129 | 27 | 93.1 | 297 | 10 | AF544566 | AF544566 | HIV-1 | iso |
| 130 | 27 | 93.1 | 297 | 10 | AF544571 | AF544571 | HIV-1 | iso |
| 131 | 27 | 93.1 | 297 | 10 | AF544590 | AF544590 | HIV-1 | iso |
| 132 | 27 | 93.1 | 297 | 10 | AF544611 | AF544611 | HIV-1 | iso |
| 133 | 27 | 93.1 | 297 | 10 | AY182828 | AY182828 | HIV-1 | iso |
| 134 | 27 | 93.1 | 297 | 10 | AY203678 | AY203678 | HIV-1 | iso |
| 135 | 27 | 93.1 | 297 | 10 | AY203680 | AY203680 | HIV-1 | iso |
| 136 | 27 | 93.1 | 297 | 10 | AY203681 | AY203681 | HIV-1 | iso |
| 137 | 27 | 93.1 | 297 | 10 | AY203682 | AY203682 | HIV-1 | iso |
| 138 | 27 | 93.1 | 297 | 10 | AY203683 | AY203683 | HIV-1 | iso |
| 139 | 27 | 93.1 | 297 | 10 | AY203685 | AY203685 | HIV-1 | iso |
| 140 | 27 | 93.1 | 297 | 10 | AY203687 | AY203687 | HIV-1 | iso |
| 141 | 27 | 93.1 | 297 | 10 | AY203688 | AY203688 | HIV-1 | iso |
| 142 | 27 | 93.1 | 297 | 10 | AY203689 | AY203689 | HIV-1 | iso |
| 143 | 27 | 93.1 | 297 | 10 | AY305996 | AY305996 | HIV-1 | iso |
| 144 | 27 | 93.1 | 297 | 10 | AY305999 | AY305999 | HIV-1 | iso |
| 145 | 27 | 93.1 | 297 | 10 | AY313344 | AY313344 | HIV-1 | iso |
| 146 | 27 | 93.1 | 297 | 10 | AY370055 | AY370055 | HIV-1 | iso |
| 147 | 27 | 93.1 | 297 | 10 | AY370057 | AY370057 | HIV-1 | iso |
| 148 | 27 | 93.1 | 297 | 10 | AY455412 | AY455412 | HIV-1 | iso |
| 149 | 27 | 93.1 | 297 | 10 | AY502098 | AY502098 | HIV-1 | iso |
| 150 | 27 | 93.1 | 297 | 10 | AY569833 | AY569833 | HIV-1 | iso |

ALIGNMENTS

RESULT 1

FCU06650

LOCUS FCU06650 658 bp RNA linear VRL 24-MAY-1995

DEFINITION Feline calicivirus FS capsid protein gene, partial cds.

ACCESSION U06650

SCORE Search Results Details for Application 10763712 and Search Result us-10-763-712b-186.rge.

Comments /
Suggestions

start

[Go Back to previous page](#)

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: June 29, 2006, 19:33:54 ; Search time 2257.33 Seconds
(without alignments)
339.945 Million cell updates/sec

```
Title:          US-10-763-712B-186
Perfect score:  29
Sequence:       1 ADXTIXEE 8
```

```
Scoring table:  BLOSUM62
                  Xgapop 10.0 , Xgapext 0.5
                  Ygapop 10.0 , Ygapext 0.5
                  Fgapop  6.0 , Fgapext 7.0
                  Delop  6.0 , Delext  7.0
```

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 150 summaries
```

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Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/abss/ABSSWEB_spool/US10763712/runat_29062006_075057_19242/app_query.fasta_1
-DB=GenEmbl -QFMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=150
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=25 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss05h
-USER=US10763712_@CGN_1_1_5767_@runat_29062006_075057_19242 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
```

```
Database :      GenEmbl:*
           1:  gb env:*
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2: gb_pat:*
 3: gb_ph:*
 4: gb_pl:*
 5: gb_pr:*
 6: gb_ro:*
 7: gb_sts:*
 8: gb_sy:*
 9: gb_un:*
 10: gb_vi:*
 11: gb_ov:*
 12: gb_htg:*
 13: gb_in:*
 14: gb_om:*
 15: gb_ba:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result | No. | Score | % Query Match | Length | DB | ID | Description |
|--------|-----|-------|---------------------|--------|----|------------|--------------------|
| | 1 | 29 | 100.0 | 658 | 10 | FCU06650 | U06650 Feline cali |
| | 2 | 29 | 100.0 | 1098 | 13 | DROPENFSB | M15765 D.melanogas |
| | 3 | 29 | 100.0 | 1619 | 2 | CQ579063 | CQ579063 Sequence |
| | 4 | 29 | 100.0 | 1620 | 13 | DMU13178 | U13178 Drosophila |
| | 5 | 29 | 100.0 | 1652 | 13 | BT004875 | BT004875 Drosophil |
| | 6 | 29 | 100.0 | 1657 | 13 | DRORNABP | L37083 Drosophila |
| c | 7 | 29 | 100.0 | 6664 | 2 | CQ579062 | CQ579062 Sequence |
| c | 8 | 29 | 100.0 | 81181 | 12 | AC019668 | AC019668 Drosophil |
| c | 9 | 29 | 100.0 | 110000 | 12 | AP006485_0 | AP006485 Cyanidios |
| c | 10 | 29 | 100.0 | 155728 | 6 | AC139325 | AC139325 Mus muscu |
| c | 11 | 29 | 100.0 | 169623 | 6 | AC131581 | AC131581 Mus muscu |
| | 12 | 29 | 100.0 | 176969 | 13 | AC010707 | AC010707 Drosophil |
| | 13 | 29 | 100.0 | 192540 | 13 | AC010846 | AC010846 Drosophil |
| | 14 | 29 | 100.0 | 195753 | 12 | AC128091 | AC128091 Rattus no |
| | 15 | 29 | 100.0 | 206259 | 12 | AC156218 | AC156218 Bos tauru |
| c | 16 | 29 | 100.0 | 227299 | 6 | AC138722 | AC138722 Mus muscu |
| c | 17 | 29 | 100.0 | 242568 | 12 | AC134100 | AC134100 Rattus no |
| | 18 | 29 | 100.0 | 295650 | 15 | BX294151 | BX294151 Pirellula |
| | 19 | 29 | 100.0 | 323840 | 13 | AE003501 | AE003501 Drosophil |
| | 20 | 28 | 96.6 | 144 | 10 | S61103 | S61103 gag [avian |
| c | 21 | 28 | 96.6 | 280 | 14 | AB104398 | AB104398 Equus cab |
| c | 22 | 28 | 96.6 | 810 | 7 | BV655660 | BV655660 S217P6913 |
| | 23 | 28 | 96.6 | 3212 | 5 | BC038232 | BC038232 Homo sapi |
| | 24 | 28 | 96.6 | 3566 | 4 | AK065392 | AK065392 Oryza sat |
| c | 25 | 28 | 96.6 | 3807 | 4 | AK069356 | AK069356 Oryza sat |
| | 26 | 28 | 96.6 | 4433 | 6 | AK129390 | AK129390 Mus muscu |
| | 27 | 28 | 96.6 | 4706 | 2 | CQ715465 | CQ715465 Sequence |
| | 28 | 28 | 96.6 | 5264 | 2 | DD210151 | DD210151 Methods o |
| | 29 | 28 | 96.6 | 5323 | 2 | AR578550 | AR578550 Sequence |
| | 30 | 28 | 96.6 | 6395 | 5 | AB046769 | AB046769 Homo sapi |
| | 31 | 28 | 96.6 | 7548 | 6 | BC079889 | BC079889 Mus muscu |
| c | 32 | 28 | 96.6 | 7693 | 15 | AY509036 | AY509036 Bifidobac |
| | 33 | 28 | 96.6 | 10811 | 15 | AE009306 | AE009306 Agrobacte |
| c | 34 | 28 | 96.6 | 10924 | 15 | AE008308 | AE008308 Agrobacte |
| | 35 | 28 | 96.6 | 12393 | 15 | AE012414 | AE012414 Xanthomon |
| c | 36 | 28 | 96.6 | 14000 | 2 | CQ800374 | CQ800374 Sequence |
| | 37 | 28 | 96.6 | 37225 | 13 | CEC17E4 | Z81037 Caenorhabdi |

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| c | 38 | 28 | 96.6 | 37302 | 5 | D87007 | D87007 Homo sapien |
| c | 39 | 28 | 96.6 | 43594 | 5 | AC093144 | AC093144 Homo sapi |
| | 40 | 28 | 96.6 | 43840 | 13 | CBRG45G04 | AC084633 Caenorhab |
| c | 41 | 28 | 96.6 | 106247 | 12 | AC121232 | AC121232 Medicago |
| | 42 | 28 | 96.6 | 110000 | 4 | AP008212_284 | Continuation (285 |
| c | 43 | 28 | 96.6 | 110000 | 4 | CR382123_12 | Continuation (13 o |
| c | 44 | 28 | 96.6 | 110000 | 4 | CR382133_01 | Continuation (2 of |
| | 45 | 28 | 96.6 | 110000 | 12 | AC129397_0 | AC129397 Rattus no |
| | 46 | 28 | 96.6 | 110000 | 12 | CT005269_11 | Continuation (12 o |
| | 47 | 28 | 96.6 | 110000 | 15 | CP000076_18 | Continuation (19 o |
| c | 48 | 28 | 96.6 | 110000 | 15 | AY596297_05 | Continuation (6 of |
| c | 49 | 28 | 96.6 | 115996 | 4 | AC146566 | AC146566 Medicago |
| c | 50 | 28 | 96.6 | 128946 | 12 | AP007875 | AP007875 Lotus cor |
| c | 51 | 28 | 96.6 | 132114 | 5 | AC026772 | AC026772 Homo sapi |
| | 52 | 28 | 96.6 | 137590 | 12 | AC027567 | AC027567 Homo sapi |
| | 53 | 28 | 96.6 | 140682 | 5 | HS283K11 | AL024497 Human DNA |
| | 54 | 28 | 96.6 | 143376 | 5 | AC012331 | AC012331 Homo sapi |
| c | 55 | 28 | 96.6 | 144430 | 5 | AC091155 | AC091155 Homo sapi |
| c | 56 | 28 | 96.6 | 146903 | 12 | AC024410 | AC024410 Homo sapi |
| c | 57 | 28 | 96.6 | 151111 | 5 | AC002308 | AC002308 Homo sapi |
| | 58 | 28 | 96.6 | 156495 | 12 | AL157374 | AL157374 Homo sapi |
| | 59 | 28 | 96.6 | 163648 | 12 | AC142370 | AC142370 Rattus no |
| | 60 | 28 | 96.6 | 166128 | 4 | AP005457 | AP005457 Oryza sat |
| | 61 | 28 | 96.6 | 168509 | 5 | AC009837 | AC009837 Homo sapi |
| | 62 | 28 | 96.6 | 169514 | 12 | CT027648 | CT027648 Danio rer |
| | 63 | 28 | 96.6 | 170250 | 6 | AC144648 | AC144648 Mus muscu |
| c | 64 | 28 | 96.6 | 173485 | 11 | CR388028 | CR388028 Zebrafish |
| c | 65 | 28 | 96.6 | 174851 | 12 | AC173325 | AC173325 Bos tauru |
| c | 66 | 28 | 96.6 | 176015 | 6 | AC164003 | AC164003 Mus muscu |
| | 67 | 28 | 96.6 | 177220 | 6 | AC102550 | AC102550 Mus muscu |
| c | 68 | 28 | 96.6 | 178146 | 12 | AC121453 | AC121453 Rattus no |
| | 69 | 28 | 96.6 | 179273 | 12 | AC134386 | AC134386 Papio anu |
| c | 70 | 28 | 96.6 | 186505 | 12 | CT583651 | CT583651 Danio rer |
| | 71 | 28 | 96.6 | 188342 | 6 | AC173966 | AC173966 Mus muscu |
| c | 72 | 28 | 96.6 | 200300 | 12 | AC111531 | AC111531 Rattus no |
| | 73 | 28 | 96.6 | 206878 | 6 | AC157667 | AC157667 Mus muscu |
| c | 74 | 28 | 96.6 | 211684 | 6 | AC147637 | AC147637 Mus muscu |
| | 75 | 28 | 96.6 | 218522 | 6 | AC154806 | AC154806 Mus muscu |
| | 76 | 28 | 96.6 | 224461 | 12 | AC115419 | AC115419 Rattus no |
| c | 77 | 28 | 96.6 | 225586 | 11 | BX469934 | BX469934 Zebrafish |
| c | 78 | 28 | 96.6 | 228760 | 12 | AC129816 | AC129816 Rattus no |
| c | 79 | 28 | 96.6 | 228976 | 11 | AC144489 | AC144489 Gasterost |
| c | 80 | 28 | 96.6 | 230334 | 6 | AC112521 | AC112521 Mus muscu |
| c | 81 | 28 | 96.6 | 233946 | 6 | AC156790 | AC156790 Mus muscu |
| c | 82 | 28 | 96.6 | 236791 | 6 | AC167013 | AC167013 Mus muscu |
| c | 83 | 28 | 96.6 | 237455 | 12 | AC096815 | AC096815 Rattus no |
| | 84 | 28 | 96.6 | 249667 | 12 | AC114720 | AC114720 Rattus no |
| c | 85 | 28 | 96.6 | 269263 | 12 | AC097883 | AC097883 Rattus no |
| | 86 | 28 | 96.6 | 294850 | 15 | BX294148 | BX294148 Pirellula |
| | 87 | 28 | 96.6 | 308916 | 2 | CQ870470 | CQ870470 Sequence |
| | 88 | 27 | 93.1 | 252 | 10 | AY797550 | AY797550 HIV-1 iso |
| | 89 | 27 | 93.1 | 255 | 10 | AY797637 | AY797637 HIV-1 iso |
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| | 94 | 27 | 93.1 | 283 | 10 | AY335008 | AY335008 HIV-1 iso |
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| | 97 | 27 | 93.1 | 288 | 10 | AY370056 | AY370056 HIV-1 iso |
| | 98 | 27 | 93.1 | 294 | 10 | AY797136 | AY797136 HIV-1 iso |

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| 99 | 27 | 93.1 | 296 | 10 | AF291129 | AF291129 | HIV-1 | iso |
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| 104 | 27 | 93.1 | 297 | 10 | AF142229 | AF142229 | HIV-1 | fro |
| 105 | 27 | 93.1 | 297 | 10 | AF142231 | AF142231 | HIV-1 | fro |
| 106 | 27 | 93.1 | 297 | 10 | AF142232 | AF142232 | HIV-1 | fro |
| 107 | 27 | 93.1 | 297 | 10 | AF142233 | AF142233 | HIV-1 | fro |
| 108 | 27 | 93.1 | 297 | 10 | AF142234 | AF142234 | HIV-1 | fro |
| 109 | 27 | 93.1 | 297 | 10 | AF142235 | AF142235 | HIV-1 | fro |
| 110 | 27 | 93.1 | 297 | 10 | AF142236 | AF142236 | HIV-1 | fro |
| 111 | 27 | 93.1 | 297 | 10 | AF142238 | AF142238 | HIV-1 | fro |
| 112 | 27 | 93.1 | 297 | 10 | AF142239 | AF142239 | HIV-1 | fro |
| 113 | 27 | 93.1 | 297 | 10 | AF204326 | AF204326 | HIV-1 | pat |
| 114 | 27 | 93.1 | 297 | 10 | AF204368 | AF204368 | HIV-1 | pat |
| 115 | 27 | 93.1 | 297 | 10 | AF227687 | AF227687 | HIV-1 | pat |
| 116 | 27 | 93.1 | 297 | 10 | AF227688 | AF227688 | HIV-1 | pat |
| 117 | 27 | 93.1 | 297 | 10 | AF288796 | AF288796 | HIV-1 | iso |
| 118 | 27 | 93.1 | 297 | 10 | AF288797 | AF288797 | HIV-1 | iso |
| 119 | 27 | 93.1 | 297 | 10 | AF288804 | AF288804 | HIV-1 | iso |
| 120 | 27 | 93.1 | 297 | 10 | AF311132 | AF311132 | HIV-1 | iso |
| 121 | 27 | 93.1 | 297 | 10 | AF317024 | AF317024 | HIV-1 | GR. |
| 122 | 27 | 93.1 | 297 | 10 | AF544416 | AF544416 | HIV-1 | iso |
| 123 | 27 | 93.1 | 297 | 10 | AF544475 | AF544475 | HIV-1 | iso |
| 124 | 27 | 93.1 | 297 | 10 | AF544509 | AF544509 | HIV-1 | iso |
| 125 | 27 | 93.1 | 297 | 10 | AF544519 | AF544519 | HIV-1 | iso |
| 126 | 27 | 93.1 | 297 | 10 | AF544554 | AF544554 | HIV-1 | iso |
| 127 | 27 | 93.1 | 297 | 10 | AF544556 | AF544556 | HIV-1 | iso |
| 128 | 27 | 93.1 | 297 | 10 | AF544560 | AF544560 | HIV-1 | iso |
| 129 | 27 | 93.1 | 297 | 10 | AF544566 | AF544566 | HIV-1 | iso |
| 130 | 27 | 93.1 | 297 | 10 | AF544571 | AF544571 | HIV-1 | iso |
| 131 | 27 | 93.1 | 297 | 10 | AF544590 | AF544590 | HIV-1 | iso |
| 132 | 27 | 93.1 | 297 | 10 | AF544611 | AF544611 | HIV-1 | iso |
| 133 | 27 | 93.1 | 297 | 10 | AY182828 | AY182828 | HIV-1 | iso |
| 134 | 27 | 93.1 | 297 | 10 | AY203678 | AY203678 | HIV-1 | iso |
| 135 | 27 | 93.1 | 297 | 10 | AY203680 | AY203680 | HIV-1 | iso |
| 136 | 27 | 93.1 | 297 | 10 | AY203681 | AY203681 | HIV-1 | iso |
| 137 | 27 | 93.1 | 297 | 10 | AY203682 | AY203682 | HIV-1 | iso |
| 138 | 27 | 93.1 | 297 | 10 | AY203683 | AY203683 | HIV-1 | iso |
| 139 | 27 | 93.1 | 297 | 10 | AY203685 | AY203685 | HIV-1 | iso |
| 140 | 27 | 93.1 | 297 | 10 | AY203687 | AY203687 | HIV-1 | iso |
| 141 | 27 | 93.1 | 297 | 10 | AY203688 | AY203688 | HIV-1 | iso |
| 142 | 27 | 93.1 | 297 | 10 | AY203689 | AY203689 | HIV-1 | iso |
| 143 | 27 | 93.1 | 297 | 10 | AY305996 | AY305996 | HIV-1 | iso |
| 144 | 27 | 93.1 | 297 | 10 | AY305999 | AY305999 | HIV-1 | iso |
| 145 | 27 | 93.1 | 297 | 10 | AY313344 | AY313344 | HIV-1 | iso |
| 146 | 27 | 93.1 | 297 | 10 | AY370055 | AY370055 | HIV-1 | iso |
| 147 | 27 | 93.1 | 297 | 10 | AY370057 | AY370057 | HIV-1 | iso |
| 148 | 27 | 93.1 | 297 | 10 | AY455412 | AY455412 | HIV-1 | iso |
| 149 | 27 | 93.1 | 297 | 10 | AY502098 | AY502098 | HIV-1 | iso |
| 150 | 27 | 93.1 | 297 | 10 | AY569833 | AY569833 | HIV-1 | iso |

ALIGNMENTS

RESULT 1

FCU06650

LOCUS FCU06650 658 bp RNA linear VRL 24-MAY-1995

DEFINITION Feline calicivirus FS capsid protein gene, partial cds.

ACCESSION U06650

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